

1397

351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
 401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
 451 TLADTSPEYA YRVTLDRHNR LQWHPATRK TYPNEPEAKL WKRIA AKILS
 501 LPIESLL*

m987/a987 98.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987.pep	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY					
a987	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m987.pep	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAAERGVRVRLLLDDN					
a987	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAAERGVRVRLLLDDN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m987.pep	NTRGLDDLLALDHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
a987	NTRGLDDLLALDHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m987.pep	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGDIG					
a987	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m987.pep	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVRTRLISDDPAKGLDRDR					
a987	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDDPAKGLDRDR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m987.pep	RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGDIDVTLTNSLQATDVA					
a987	RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGDIDVTLTNSLQATDVA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m987.pep	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
a987	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
	370	380	390	400	410	420
	430	440	450	460	470	480
m987.pep	SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPAYAYRVTLDRHNRQLQWHPATRK					
a987	SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTSPEYAYRVTLDRHNRQLQWHPATRK					
	430	440	450	460	470	480
	490	500	509			
m987.pep	TYPNEPEAKLWKRIA AKILSLLPIEGLLX					
a987	TYPNEPEAKLWKRIA AKILSLLPIESLLX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2979>:

g988.seq
 1 ATGAATAAAA ATATTAATC TTAAATTTA CGGGAAAAAG ACCCGTTTTT

1398

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51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCCAGT CGGgaATGGA
101 TAATCGAATT GTTGGAGCGC AAAGGTGTGC CTTCAAAAAT CGAATCGCTT
151 GCACGCGAGC TGTCGATTAC GGAAGacgaq tATGTCTTTT TTGAACGCCG
201 TCTGAaggCG atgGCGCGGG AcggtCAGGT TTTAATCAAC CGCCgaggcg
251 CagtTTGCGc gGCGgacaag ctgGATTGCG TCAAAATGccg Cctcgaggcg
301 catAAgGAcg gtttcggctt cgcCGTGCCG CTCATGCCGA TGGACGAAGG
351 GGATTTTCGTT TTATACGAAC GCCAgatgcg tggTgtcatG CAcgcgaca
401 ccggttACCGT CCGTCCTGCG ggtatggaCC GCAGGGGccg ccgcGAAGgg
451 acgttttctGG ATATTGTCGA ACGCGCGCAA AGCAAAGTTG TCGGCCGTTT
501 CTATATGGAT AGGGGCGTGG CGATTTTGA GCGGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTGTGGA CCGGACGGCG TGGCGCGTTT CAAACCGGAA
601 TCCGGTCAGG TTATCGTCGG CAAAATTGAG GTTTATCCCG AGCAAAACCG
651 GCCTGCAGTG GCAAAAATCA TTGAAGTTTT GGGCGATTAT GCCGACAGCG
701 GGATGGAAt cgAAATTGCC GTGCGCAAGC ATCATTTGCC GCaccgaTTC
751 AGTGAagcgt gtGcCAAATC CGcgaAAAA ATtcccgaac ATGTACGCAA
801 AAGCGATTG AAAGGCCGCG TCGATTGTG CGACCTTCCT TTGGTAACGA
851 TAGACGGCGA AACGGCGCGC GATTTTCGAC ACGCGGTGTT TGCCGGAATA
901 CTCGGACGCA ATTACCGCCT GGTCTGGCG ATTGCGGATG TCAGCCATTA
951 TGTCCGCCCT GACGATGCGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
1001 GCGTGTATTT CCCGCGCCGT ATGATTCCGA TGCTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
1101 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTATC
1151 CCGCCGTGAT GCGCTCTCAT GCCCGCTGA CCAAGTGA AGTTTGGA
1201 TGGCTTTCAG ACGGCATCGG GAATCGCAC AAAGCCCAAA TCGACACGCT
1251 TTACAAGCTG TTTAAATTT TGCAGAAAAA ACGTCTGGCG CGCGGGCGG
1301 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGACGA CAACGGCAAA
1351 ATCGAAAAA TTGTCCCGT CGTCCGCAAC gatGCCCCA AGCTGATTGA
1401 AGAATGTATG CTGGCGGCGA ATGTTTGGCG GCGCGATTTT CTGTTGAAAA
1451 ACAACATAC GGCTTTGTTC CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1501 CTCGCCACCC TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1551 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GAACAATTCA
1601 AAGGCAGGCC GGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAGCAGGCGG TTTACGAACC GCATTGCGAA GGGCATTTCG GTTTGGCTTA
1701 TGAAGCATAC GCCCACTTTA CCTCGCCCAT CCGCGCTAT CCCGACCTGA
1751 CCGTCCACCG TGCCATCAAA GCCGTATTGA ACCGGAAAAC CTACACGCCA
1801 AACAAAGCT GGCAGGCTTT GGGCGTGCAT ACTTCGTTTT GCGAACGCCG
1851 TGCCGACGAT GCTGGCCGCG ATGTGGAAAA CTGGCTGAAA ACTTATTATA
1901 TGCGCGATAA GGTGCGTGAA ATATTGAAG GcaaaatCtc ccggggtgtg
1951 gcaaaTtttg gaATATTTGT CACTTTGGAC GATATccata tcgacggtct
2001 ggtacaTATC AGCGatttg gcaAGATTA TTTCaacttc cgcgccgAAA
2051 TCATGGCAAT CGAAGGCGAA CGCAGCGGCA TCCGTTTCAA TATGGGGGAC
2101 AGGGTTGCCG TCCGGGTCGC GCGTGCCGAT TTGGATGATG GAAAAATCGA
2151 CTTTGTCTTA ATTGCGGAG AAAGCGGCG GCGGCGGAAG GTCAAATTAT
2201 CCGCATCTGC CAAACCGGCA GGGGCGGCG GGAAGGGAA ATCGAAAACC
2251 ACCGCCGAGA AAAAAACAGC CCGATGCGGC AAAGTAAGGG GAAGGGGCGT
2301 GCCTGCCGTT GCCGAATCGG GAAAAAGGC AAAGAAACCG GTTCCGATTA
2351 AGGTCAAAAA ACGGAAAGGC AAATCATAA

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This corresponds to the amino acid sequence <SEQ ID 2980; ORF 988.ng>:

g988.pep

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1  MNKNIKSLNL REKDPFLSRE KQRYEHLPLS REWIIELLER KGVPSKIESL
51  ARELSITEDE YVFFERRLKA MARDGOVLIN RRGAVCAADK LDLVKRVEA
101 HKDGFGEFAP LMPMDEGDFV LYERQMRGVM HGDVTVTRPA GMDRRGRREG
151 TFLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
201 SGQVIVGKIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPFRF
251 SEACAKSAKK IPDHVRKSDL KGRVDLCDLP LVTIDGETAR DFDDAVFAEK
301 VGRNYRLVVA IADVSHYVRP DDAIDADAQE RSTSVYFPRR MIPMLPENLS
351 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
401 WLSDGIGNPH KAQIDTLYKL FKILQKKRLA RGAVEFESVE TQMIFFDNGK
451 IEKIVPVVRN DAHLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LATLREQLGL LGLQLGGGDN PSPKDYAALA EQFKGRPD AE LLQVMMLRSM
551 QQAVYEPHCE GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNRKTYTP
601 NKSQALGVH TSFCERRADD AGRDVENWLK TTYMRDKVGE IFEGKISRGV
651 ANFGIFVTL DDIHIDGLVHI SDLGEDYFNF RPEIMAEIET RSGIRFNMGD
701 RVAVRVARAD LDDGKIDFVL IAGESGRRRK VKLSASAKPA GAAGKGKSKT
751 TAEKKTARCG KVRGRGVPAV AESGKKAKKP VPIIYKKRKG KS*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2981>:

```
m988.seq (partial)
1  ..ACAGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCCGTTT
51  CTATATGGAT AGGGGCGTGG CGATTTTGGG GCCGGAAGAC AAGCGTCTGA
101 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
151 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
201 GCCGGCAGTG GCAAAAATCA TCGAAGTTT GGGCGATTAT GCCGACAGCG
251 GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
301 AGTGAAGCGT GTGCCAAAGC TCGGAAAAAA ATTCCCGTCC ATGTACGCAA
351 AAGCGATTTG AAAGGCCGCG TCGATTTGCG CGACCTGCCT TTGGTAACGA
401 TAGACGGCGA AACGGCGCGC GATTTCGACG ACGCGGTGTT TGCCGAAAAA
451 GTCGGACGCA ATTACCGTCT GGTCTGGCG ATTGCGGATG TCAGCCATTA
501 TGTCCGCCCT GACGATGTGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
551 GCGTATATTT CCCGCGCCGT GTGATTCCGA TGCTGCCGGA AAACCTGTCT
601 AACGGCATTT GCTCGCTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
651 CGATATGGTC GTTACCTATG CCGGCAATAT CAAAGAATAC CGCTTCTACC
701 CCGCCGTAAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGGAAA
751 TGGATTTTCA ACGGCATCGA CCATCCGTAC AAAGCCCAAA TCGACACCCCT
801 TTACAAACTC TTCAAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGCGCGG
851 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGATGA CAACGGCAAA
901 ATCGAAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCCACA AGCTGATTGA
951 AGAATGTATG CTGGCGGCGA ATGTTTGCGC AGCGGATTTC CTGTTGAAAA
1001 ACAAGCATA C GGCTTTGTTC CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1051 CTCGCCACCC TGCGCGAGCA GCTCGGTCG TTTGGGGCTT AACTTGGCGG
1101 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGTC GAACAATTCA
1151 AAGGCAGACC TGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1201 CAGCAGGCGG TTTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCCTA
1251 CGAAGCATA C GCCCCTTCA CCTCGCCAT CCGCCGCTAT CCGGACCTGA
1301 CCGTACACCG CGCCATCAA GCGGTGTTGA ATCAGCAAAC CTACACGCCA
1351 AAAAAAAGCT GGCAGGCTTT GGGCGTGCAT AUCTCGTTCT GTGAGCGCGG
1401 TGCCGACGAC GCCAGCCGCG ACGTGGAAAA CTGGCTGAAA ACCTATTATA
1451 TGCGCGATAA GGTGCGCGAA GTATTGAA G TAAAATCTC CGGCATGACC
1501 AGTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
1551 GCATATCAGC GATTTGGGCG AAGACTATTT CAACTTCCGC CCCGAAATCA
1601 TGGCAATCGA AGGCGAACGC AGCGCATCC GTTCAACAT GGGGGACAGG
1651 GTTGGCGTCC GGGTCGCCCC TGCCGATTTG GATGACGGAA AAATCGATTT
1701 TGTCTGATT GCCGGGGGGA GCGGCAGGGG GCGGAAAGTT AAATCATCCG
1751 CGTCTGCCAA ACCGGCAGGG ACGGCGGGGA AAGGGAAGCC GAAACCGGCC
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1400

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1801   GCCGAGAAAA AAACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGCGCGCTC
1851   TGCCGCCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAGG
1901   TAAAAAACG GAAAGGCAAA TCATAA

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This corresponds to the amino acid sequence <SEQ ID 2982; ORF 988>:

```

m988.pep (partial)
1   ..TVLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
51  SGQVIVGEIE VYPEQNRPAV AKIEVLGDY AD SGMEIEIA VRKHHLPHQF
101 SEACAKAAKK IPVHVRKSDL KGRVDLRDLP LVTIDGETAR DFDDAVFAEK
151 VGRNYRLVVA IADVSHYVRP DDVIDADAQE RSTSVYFPRR VIPMLPENLS
201 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY F FYPVMRSH ARLTYNQVWK
251 WISDGIDHPY KAQIDTLYKL FKILQKKRFE AGAVEFESVE TQMIFDDNGK
301 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
351 LATLREQQLG LGLQLGGGDN PSPKDYAALV EQFKGRPD AE LLOVMMLRSM
401 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQQTYP
451 KKSQWALGVH TSFCERRADD ASRDVENWLK TTYMRDKVGE VFEGKISGMT
501 SFGIFVTLDG IHIDGLVHIS DLGEDYFNFR PEIMAEGER SGIRFNMGDR
551 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGKPKTA
601 AEKKTARGGK VRGRGASAAA ESRKKAKKPV PIKVKKRKGK S*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m988/g988 94.2% identity in 642 aa overlap

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m988.pep                                     10      20      30
                                         TVLDIVERAQSKVVGRFYMDRGVAILEPED
g988      LYERQMRGVMHGDTVTVRPAGMDRRGRREGTFLDIVERAQSKVVGRFYMDRGVAILEPED
              130      140      150      160      170      180

m988.pep              40      50      60      70      80      90
KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIEVLGDYADSGMEIEIA
g988      KRLNQSIVLEPDGVARFKPESGQVIVGKIEVYPEQNRPAVAKIEVLGDYADSGMEIEIA
              190      200      210      220      230      240

m988.pep              100      110      120      130      140      150
VRKHHLPHQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLP LVTIDGETARDFDDAVFAEK
g988      VRKHHLPHRFSEACAKSAKKIPDHVRKSDLKGRVDLCDLPLVTIDGETARDFDDAVFAEK
              250      260      270      280      290      300

m988.pep              160      170      180      190      200      210
VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFPRRVIPMLPENLSNGICSLNPDV
g988      VGRNYRLVVAIADVSHYVRPDDAIDADAQERSTSVYFPRRMIPMLPENLSNGICSLNPDV
              310      320      330      340      350      360

m988.pep              220      230      240      250      260      270
ERLCMVCDMVVTYAGNIKEYRFYPVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL
g988      ERLCMVCDMVVTYAGNIKEYRFYPVMRSHARLTYNQVWKWISDGIGNPHKAQIDTLYKL
              370      380      390      400      410      420

m988.pep              280      290      300      310      320      330
FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF
g988      FKILQKKRLARGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF
              430      440      450      460      470      480

m988.pep              340      350      360      370      380      390
LLKNKHTALFRNHLGPTPEKLATLREQLLGLQLGGGDNPSPKDYAALVEQFKGRPD AE
g988      LLKNKHTALFRNHLGPTPEKLATLREQLLGLQLGGGDNPSPKDYAALVEQFKGRPD AE

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1401

	490	500	510	520	530	540
	400	410	420	430	440	450
m988.pep	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQOITYTP					
g988	LLQVMMLRSMQQAVYEPHCEGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNKRKITYTP					
	550	560	570	580	590	600
	460	470	480	490	500	509
m988.pep	KKSQWQALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEKGKIS-GMTSFGIFVTLTD					
g988	NKSQWQALGVHTSFCERRADDAGRDVENWLKTYMRDKVGEIFEKGKISRGVANFGIFVTLTD					
	610	620	630	640	650	660
	510	520	530	540	550	569
m988.pep	GIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVI					
g988	DIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVL					
	670	680	690	700	710	720
	570	580	590	600	610	629
m988.pep	IAGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKKTARGGKVRGRGASAAAESRKKAKKP					
g988	IAGESGRRRKVKLSASAKPAGAAGKGSKTTAEKKKTARCGKVRGRGVPAAVESGKKAKKP					
	730	740	750	760	770	780
	630	640				
m988.pep	VPIKVKKRKGKXS					
g988	VPIKVKKRKGKXS					
	790					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2983>:

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a988.seq
1  ATGAATAAAA ATATTAATC TTTAAATTTA CGGGAAAAAG ACCCGTTTTT
51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCAGT CGGGAATGGA
101 TAATCGAGCT GCTTGAACGT AAAGGCGTAC CATCCAAGAT TGAAGCTTTG
151 GTACGCGAAT TGTGCGATTAA GGAAGAAGAG TACGAATTTT TCGAACGTCG
201 TCTGAAGGCG ATGGCGCGGG ACGGTCAGGT TTTAATCAAC CGTCGGGGCG
251 CGGTTTGCGC GGCGGACAAA TTGGATTGCG TCAAATGCCG TGTCAAGGCG
301 CACAAAGACC GCTTCGGTTT CGCGGTGCCG CTCACGCCCG CCAAAGACGG
351 TGATTTTGTC TTGTACGAAC GCCAGATGCG CGGCATTATG CACGGCGATA
401 TTGTCACTGT TCGTCTGCC GGCATGGACG GTAGGGGCGG CCGCGAAGGG
451 ACGGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
501 CTANATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
601 TCCGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
651 GCCGGCAGTG GCAAAAATCA TCGAAGTTT GGGCGATTAT GCCGACAGCG
701 GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
751 AGTGAAGCGT GTGCCAAAGC CGCGAAAAAA ATTCCCGACC ATGTACGCAA
801 AAGCGATTG AAAGGCCGCG TCGATTTGCG CGACCTGCCT TTGGTAACGA
851 TAGACGGCGA AACGGCTCGA GATTTTGACG ATGCGGTGTT TGCCGAGAAA
901 ATCGGACGCA ATTACCGTCT GGTGCTGGCG ATTGCCGATG TCAGCCATTA
951 TGTCCGCCCC GATGACGCTA TCGACACGGA CGCTCAGGAA CGCAGCACCA
1001 GTGTTTACTT CCCGCGCCGC GTGATTCCCA TGTGCGCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCTCATGTC GAGCGTTTGT GTGTGGTGTG
1101 CGATATGGTT ATCACTTACG CGGGCAATAT CAAAGAATAC CGCTTCTACC
1151 CCGCCGTGAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGGAAA
1201 TGGCTTTCAG GCGGCATCGA GCATCCGTTT AAACCCAAA TCGACACGCT
1251 TTACAAATCT TTCAAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGGGCGG
1301 TGGAGTTTGA CAGCATCGAA ACCCAAATGC TTTTCGACGA CAACGGTAAA
1351 ATTGAAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCCA CAAGCTGATTGA
1401 AGAATGTATG TTGGCGGCAA ACGTTTGGCG AGCGGATTTT CTGTTGAAAA
1451 ACAAGCATAC CGCATTTGTC CGCAACCAT TGGGGCCAC GCCCGAAAAA
1501 CTCGCCGCT TCGCGGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1551 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GGACAGTTCA

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1402

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1601 AAGGCAGGCC GGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAACAGGCGG TTTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCTTA
1701 CGAAGCATAC GCCCACTTCA CCTCGCCCAT CCGCCGCTAT CCGACCTGA
1751 CCGTACACCG CGCCATCAAA GCCGTGTTGA ATCAGCAAAC CTACACGCCA
1801 AAAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1851 TGCCGACGAC GCCAGCCGCG ACGTGGAAAA CTGGCTGAAA ACCTATTATA
1901 TGCGCGATAA GGTCGGCGAA GTATTGCAAG GTAAAAATCT CCGCATGACC
1951 AGTTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
2001 GCATATCAGC GATTTGGGCG AAGACTATTT CAACTCCGC CCCGAAATCA
2051 TGGCAATCGA AGGCGAACGC ACGGCGATCC GTTTCACAT GGGGGACAGG
2101 GTTGCCGTCC GGGTCGCCCG TGCCGATTG GATGACGGAA AAATCGATTT
2151 TGTCTGATT GCCGGGGGGA GCGGCAGGG GCGGAAAGTT AAATCATCCG
2201 CGTCTGCCAA ACCGGCAGGG ACGGCGGGGA AAGGGAAGCC GAAACCGCC
2251 GCCGAGAAAA AAACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC
2301 TGCCGCCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAGG
2351 TAAAAAACG GAAAGGCAAA TCATAA

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This corresponds to the amino acid sequence <SEQ ID 2984; ORF 988.a>:

```

a988.pep
1 MNKNIKSLNL REKDPFLSRE KORYEHPLPS REWIELLER KGVPSKIEAL
51 VRELSIKEEE YEFFERRLKA MARDQVVLIN RRGAVCAADK LDLVKCRVKA
101 HKDRFGFAVP LTPAKDGFV LYERQMRGIM HGDIVTVRPA GMDGRGRREG
151 TVLDIVERAQ SKVVGRFXMD RGVAILPEP KRLNQSIVLE PDGVAREFKPE
201 SGQVIVGEIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPHQF
251 SEACAKAAKK IPDHVRKSDL KGRVDLRDL LVTIDGETAR DFDVAFAEK
301 IGRNYRLVVA IADVSHYVRP DDAIDTDAQE RSTSVYFPRR VIPMLPENLS
351 NGICSLNPHV ERLCVVCDMV ITYAGNIKEY RFYPVMRSH ARLTYNQVWK
401 WLSGGIEHPF KTQIDTLYKL FKILQKRFE RGAVEFDSIE TQMLFDDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LAALREQLGL LGLQLGGGDN PSPKDYAALA GQFKGRPDAE LLQVMMLRSM
551 QQAVYEFHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQOTYTP
601 KKSQWALGVH TSFCERRADD ASRDVENWLK TYYMRDKVGE VFEGKISGMT
651 SFGIFVTLDG IHIDGLVHIS DLGEDYFNFR PEIMAIEGER SGIRFNMGDR
701 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGPCKTA
751 AEKKTARGGK VRGRGASAAA ESRKKAKKPV PIKVKRKGK S*

m988/a988 97.0% identity in 641 aa overlap

m988.pep
10 20 30
TVLDIVERAQSKVVGRFYMDRQVAILPEP
|||||
a988
LYERQMRGIMHGDIVTVRPAQMDGRGRREGTVLDIVERAQSKVVGRFXMDRQVAILPEP
130 140 150 160 170 180

40 50 60 70 80 90
KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA
|||||
a988
KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA
190 200 210 220 230 240

100 110 120 130 140 150
VRKHHLPHQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLPLVTIDGETARDFDVAFAEK
|||||
a988
VRKHHLPHQFSEACAKAAKKIPDHVRKSDLKGRVDLRDLPLVTIDGETARDFDVAFAEK
250 260 270 280 290 300

160 170 180 190 200 210
VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFPRRVIPMLPENLSNGICSLNPDV
:|||||
a988
IGRNYRLVVAIADVSHYVRPDDAIDTDAQERSTSVYFPRRVIPMLPENLSNGICSLNPHV
310 320 330 340 350 360

220 230 240 250 260 270
ERLCMVCDMVITYAGNIKEYRFYPVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL
|||||
a988
ERLCVVCDMVITYAGNIKEYRFYPVMRSHARLTYNQVWKWLSGGIEHPKTKIDTLYKL

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1403

	370	380	390	400	410	420
m988.pep	280	290	300	310	320	330
	FKILQKKRFERGAVFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
a988	FKILQKKRFERGAVFDSIETQMLFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
	430	440	450	460	470	480
m988.pep	340	350	360	370	380	390
	LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGDNPSPKDYAALVEQFKGRPDAE					
a988	LLKNKHTALFRNHLGPTPEKLAALREQLGLLGLQLGGDNPSPKDYAALAGQFKGRPDAE					
	490	500	510	520	530	540
m988.pep	400	410	420	430	440	450
	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYTP					
a988	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYTP					
	550	560	570	580	590	600
m988.pep	460	470	480	490	500	510
	KKSWQALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKISGMTSFGIFVTLDG					
a988	KKSWQALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKISGMTSFGIFVTLDG					
	610	620	630	640	650	660
m988.pep	520	530	540	550	560	570
	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI					
a988	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI					
	670	680	690	700	710	720
m988.pep	580	590	600	610	620	630
	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAAESRKKAKKPV					
a988	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAAESRKKAKKPV					
	730	740	750	760	770	780
m988.pep	640					
	PIKVKKRKGKXS					
a988	PIKVKKRKGKXS					
	790					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2985>:

```

g989.seq
1  ATGACCCCTT TCACACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCTT
51  TGCCGCCGCA TCTGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCAGCGCA AATGCCGCCG ACGCGTCGAC CATCTTCTAC
151 AATCCCGCCG GCCTGACCAA ACTCGACAGC AGCCAGATTT CCGTCAACGC
201 CAACATCGTG CTGCCCAGCA TTCATTATGA AGCAGATTCC GCCACCGACT
251 TTACCGGGCT TCCCGTCCAA GGTCTAATAA ACGGCAAAAT CACCAAAACC
301 ACGGTCGCAC CCCACATTTA CGGCGCATAC AAAGTCAACG ACAATCTGAC
351 CGTGGGCTTG GCGGTGTACG TCCCTTCGG CTCTGCCACC GAATACGAAA
401 AAGATTCCGT GTTGCGCCAC AACATCAACA AACTCGGTCT GACCAGCATC
451 GCCGTGCAAC CTGTCGCCGC GTGGAACTC AACGAACGCC ATTCTTTCGG
501 CGCAGGCATC ATCGCCCAAC ATAATTCCGC CGAAGTGGC AAATATGCCG
551 ACTGAGGAAT CCCAAAAA GCGCAAATGC TGCAAGCAAC ACCTTCTAAT
601 CCTACTGCCG CTGCTCAAAT CAAGGCCGAC GGACACGCCG ATGTCAAAGG
651 CAGCGATTGG GCGCTCGGCT ACCAACTGGC GTGGATGTGG GACATCAACG
701 ACCGCGCGCG CGTGGGCGTG AACTACCGTT CCAAAGTTT ACACACGCTC
751 AAAGGCGATG CCGAATGGGC GGCAGACGGC GCGGCGGCGA AACAACAGTG
801 GAATGACAA ATGCTCACAC CGCTCGGTTA CACGGCGAAT GAAAAAGCCA
851 GTGTCAAAAT CGTAACGCCT GAGTCTTTGT CCGTACACGG CATGTACAAA

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1404

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901 GTGTCCGACA AAGCCGACCT GTTCGGCGAC GTAAC'TTGA CGCGCCACAG
951 CCGCTTCAAT AAGCGGGAAC TGTTTTTTGA AAAAGAAAAA AATATTGCTA
1001 ATGGCAAAAA ATCCGACCGC ACCACCATCA CCCCCAACTG GCGCAACACC
1051 TACAAAGTCG GCTTGGGCGG TTCTTATCAA ATCAGCGAAC CGCTGCAACT
1101 GCGCGTCGGC ATCGCTTTTG ACAAACCGCC TGTCCGCAAC GCCGACTacc
1151 GCATGAACAG CCTGCCCGAC GGCAACCGCA TCTGGTTCTC CGCCGGCATG
1201 AAATACCATA TCGGCAAAAA CCACGTCGTC GATGCCGCCT ACACCCACAT
1251 CCACATCAAC GACACCAGCT ACCGCACGGC GAAGGCAAGC GGCAACGATG
1301 TGGACAGCAA AGGTGCGTCT TCGCACGTT TCAAAAACCA CGCCGACATC
1351 ATCGGCCTGC AATACACCTA CAAATTCAAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2986; ORF 989.ng>:

```

g989.pep
  1 MTPFTLKKTV LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAADASTIFY
51 NPAGLTKLDS SQISVNANIV LPSIHYEADS ATDFTGLPVQ GSKNGKITKT
101 TVAPHIYGAY KVNDNLTVGL GVYVPFGSAT EYEKDSVLRH NINKLGLTSI
151 AVEPVAAWKL NERHSFGAGI IAQHNSAELR KYAD*GIPKK AQMLQATPSN
201 PTAAAIKAD GHADVKGSDW GVGYLAWMW DINDRARVGV NYRSKVSHTL
251 KGDAEWAADG AAAKQWQNDN MLTPLGYTAN EKASVKIVTP ESLSVHGMVK
301 VSDKADLFGD VTWTRHSRFR KAEFFFEKEK NIANGKKSDR TTITPNWRNT
351 YKVLGGGSYQ ISEPLQLRVG IAFDKPPVRN ADYRMNSLPD GNRWFSAGM
401 KYHIGKNHVV DAAYTHIHIN DTSYRTAKAS GNDVDSKGAS CAREKNHADI
451 IGLQYTYKFK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2987>:

```

m989.seq
  1 ATGACCCCTT CCGCACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCTT
51 TGCCGCCGCA TCCGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCACGGCA AATGCCGCG CCGCAGAAGC CGCCGACGCA
151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAACTCG ACAGCAGCCA
201 GATTTCCGTC AACGCCAACA TCGTGCTGCC CAGCATTCAT TATGAGGCGG
251 ATTCTCCGAC CGACTTTACC GGGCTTCCCG TCCAAGGTTT GAAAAGCGGC
301 AAAATCACCA AAACCAACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTGG GCTTGGGCGT GTACGTCCCC TTCGGCTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA
501 CCGCCATTCC TTCCGCGCAG GCATCATCGC CCAACATACT TCCGCCGAAC
551 TGCGCAAATA TGCCGACTGG GGGATTAAGA GTAAAGCAGA GATATTGACG
601 GCAAAACCGC CCAACCTAA CGGTGTAGCC GAAGCTGCAA AAATTCAGGC
651 CGACGGACAC GCCGATGTCA AAGGCAGCGA TTGGGGCTTC GGCTACCAAC
701 TGCGGTGGAT GTGGGACATC AACGACCGTG CGCGCGTGGG CGTGAATAC
751 CGTTCCAAAG TCTCGCACAC GCTCAAAGGC GATGCCGAAT GGGCGGCAGA
801 CGGCGCGGCG GCGAAAGCAA TGTGGAGTAC GATGTTGCA GCAAACGGCT
851 ACACGGCGAA TGAAAAAGCC CGCGTTAAAA TCGTTACGCC TGAGTCTTTG
901 TCCGTACACG GTATGTACAA AGTGTCCGAT AAAGCCGACC TGTTCCGCCA
951 CGTAACCTGG ACGCGCCACA GCCGCTTCGA TAAGGCGGAA CTGGTTTTTG
1001 AAAAAGAAAA AACCCTCGTC AAAGGCAAA CCGACCGCAC CACCATCACC
1051 CCCAACTGGC GCAACACCTA CAAAGTCGGC TTCGGCGGTT CTTATCAAAT
1101 CAGCGAACCG CTGCAACTGC GCGCCGCAT CGCTTTTGAC AAATCGCCCC
1151 TCCGCAACGC CGACTACCGC ATGAACAGCC TACCCGACGG CAACCGCATC
1201 TGGTTCTCCG CCGGTATGAA ATACCATATC GGTA AAAACC ACGTCGTCGA
1251 TGCCGCCTAC ACCACATCC ACATCAACGA CACCAGCTAC CGCACGGCGA
1301 AGGCAAGCGG CAACGATGTG GACAGCAAAG GCGCGTCTTC CGCACGTTTC
1351 AAAAACCACG CCGACATCAT CGGTCTGCAA TACACCTACA AATTCAAATA
1401 A

```

This corresponds to the amino acid sequence <SEQ ID 2988; ORF 989>:

```

m989.pep
  1 MTPSALKKTV LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAAAAEADA
51 STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTIVAPH IYGAYKVNDN LTVGLGVYVP FGSATEYEK SVLRHNINKL
151 GLTSIAVEPV AAWKLNDRHS FGAGIIAQHT SAELRKYADW GIKSKAEILT
201 AKPPKPNGVA EAAKIQADGH ADVKGSDFG GYQLAWMWDI NDRARVGVNY
251 RSKVSHTLKG DAEWAADGAA AKAMWSTMLA ANGYTANEKA RVKIVTPESL
301 SVHGMVKVSD KADLFGDVTW TRHSRFDKAE LVFEKEKTVV KGKSDRTTIT

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1405

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351 PNWRNTYKVG FGGSYQISEP LQLRAGIAFD KSPVRNADYR MNSLPDGNRI
401 WFSAGMKYHI GKNHVVDAA YTHIHINDTSY RTAKASGNDV DSKGASSARF
451 KNHADIIGLQ YTYKFK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

g989/m989 90.0% identity in 468 aa overlap

```

              10      20      30      40      50
g989.pep      MTPFTLKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAA-----DASTIFYNPAGL
              ||| :|||||
m989          MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL
              10      20      30      40      50      60

              60      70      80      90      100     110
g989.pep      TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKNKGITKTTVAPHIYGAYKVNND
              ||| :|||||
m989          TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNND
              70      80      90      100     110     120

              120     130     140     150     160     170
g989.pep      LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSFGAGIIAQHN
              ||| :|||||
m989          LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNRHSFGAGIIAQHT
              130     140     150     160     170     180

              180     190     200     210     220     230
g989.pep      SAELRKYADXGIPKKAQMLQATPSNPTA---AAQIKADGHADVKGSDWGVGYQLAWMWDI
              ||| :|||||
m989          SAELRKYADWGIKSAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWGFYQLAWMWDI
              190     200     210     220     230     240

              240     250     260     270     280     290
g989.pep      NDRARVGVNYSKVSHTLKGDAEWAADGAAAKQQWNDNMLTPLGYTANEKASVKIVTPES
              ||| :|||||
m989          NDRARVGVNYSKVSHTLKGDAEWAADGAAAKAMWS-TMLAANGYTANEKARVKIVTPES
              250     260     270     280     290

              300     310     320     330     340     350
g989.pep      LSVHGMKVSDKADLFGDVTWTRHSRFRNKAELFFEKEKNIANGKKSDRTTITPNWRNTYK
              ||| :|||||
m989          LSVHGMKVSDKADLFGDVTWTRHSRFDKAEVFEKEKTVVKGK-SDRTTITPNWRNTYK
              300     310     320     330     340     350

              360     370     380     390     400     410
g989.pep      VGLGGSYQISEPLQLRVGIAFDKPPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVDA
              ||| :|||||
m989          VGFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVDA
              360     370     380     390     400     410

              420     430     440     450     460
g989.pep      AYTHIHINDTSYRTAKASGNDVDSKGASCARFKNHADIIGLQYTYKFKX
              ||| :|||||
m989          AYTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX
              420     430     440     450     460

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2989>:

```

a989.seq
1   ATGACCCCTT CCGCACTGAA AAAAACCGTC CTACTGCTCG GCACTGCCTT
51  TGCCGCCGCA TCCGCACAAG CCTCCGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCAGGCA AATGCCGCCG CCGCAGAAGC CGCCGACGCA
151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAAACTCG ACAGCAGCCA
201 GATTTCGCTC AACGCCACA TCGTGCTGCC CAGCATTTCAT TATGAGGCGG
251 ATTCCGCCAC CGATTTCACC GGGCTTCCCG TCCAAGGTTT GAAAAGCGGC

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1406

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301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTAG GCTTGGGCGT GTACGTCCCC TCGGTTTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGA AACTCAACGA
501 ACGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAGC
551 TCGGCAAATA TGCCGACTGG GGGATTATGG AAAAAGCGAA AGCACTAAAA
601 GAAACACCCC CCAATCCAAC TAAAGCCGCC CAAATCAAAG CCGACGGACA
651 CGCCGATGTC AAAGGCAGCG ATTGGGGCTT CGGCTACCAA CTGGCGTGGA
701 TGTGGGACAT CAACGACCGT GCGCGCGTGG GCGTGAAC TA CCGTTCCTCAA
751 GTCTCACACA CGCTCAAAGG CGATGCCGAA TGGGCGGCAG ACGACGCAAT
801 GCGGAAACAG TTAGGGATG CAAACAAACT CGCACTGCTC GGCTACACGC
851 CAAGCGAAAA AGCCCGCGTT AAAATCGTTA CGCCCGAGTC TTTGTCCGTA
901 CACGGTATGT ACAAAGTGTC CGACAAAGCC GACCTGTTCG GCGACGTAAC
951 TTGGACGCGC CACAGCCGCT TCGATAAGGC GGAAGTGGTT TTTGAAAAAG
1001 AAAAAACCAT CGTCAACGGC AAATCCGACC GCACCAACAT CACCCCAAC
1051 TGGCGCAACA CCTACAAAGT CGGCTTCGGC GGTTCTTATC AAATCAGCGA
1101 ACCGCTGCAA CTGCGCGCCG GCATCGCTTT TGACAAATCG CCGTCCGCA
1151 ACGCCGACTA CCGCATGAAC AGCCTGCCCC ACGGCAACCG CATCTGGTTC
1201 TCCGCCGGCA TGAAATACCA TATCGGCAA AACCACGTCG TCGATGCCGC
1251 CTACACCCAC ATCCACATCA ACGACACCAG CTACCGCACG GCGAAGGCAA
1301 GCGGCAACGA TGTGGACAGC AAAGGCGCGT CTTCCGCACG TTTCAAAAA
1351 CACGCCGACA TCATCGGCCT GCAATACACC TACAAATTCA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2990; ORF 989.a>:

```

a989.pep
1  MTPSALKKTV LLLGTAFAAA SAQASGYHFG TQSVNAQSTA NAAAAEADA
51  STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYK VNDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNERHS FGAGIIAQHT SAELRKYADW GIMEKAKALK
201 ETPPNPTKAA QIKADGHADV KGS DWGFGYQ LAWMWDINDR ARVGVNYRSK
251 VSHTLKGDAE WAADDAMAKQ LWDANKLALL GYTPSEKARV KIVTPESLSV
301 HGMKYVSDKA DLFGDVTWTR HSRFDKAE LV FEKEKTIVNG KSDRTTITPN
351 WRNTYKVGFG GSYQISEPLQ LRAGIAFDKS PVRNADYRMN SLPDGNRIWF
401 SAGMKYHIGK NHVVDAAATH IHINDTSYRT AKASGNDVDS KGASSARFKN
451 HADIIGLQYT YKFK*

m989/a989 93.1% identity in 467 aa overlap

10 20 30 40 50 60
m989.pep MTPSALKKTVLLLGTAFAAAASVHASGYHFGTQSVNAQSTANAAAAEADASTIFYNPAGL
|||||
a989 MTPSALKKTVLLLGTAFAAAASQASGYHFGTQSVNAQSTANAAAAEADASTIFYNPAGL
10 20 30 40 50 60

70 80 90 100 110 120
m989.pep TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
|||||
a989 TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
70 80 90 100 110 120

130 140 150 160 170 180
m989.pep LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNRHSFGAGIIAQHT
|||||
a989 LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSFGAGIIAQHT
130 140 150 160 170 180

190 200 210 220 230 240
m989.pep SAELRKYADWGIKSKAEILTA KPPKNGVAEAAKI QADGHADVKGSDWGFGYQLAWMWDI
|||||
a989 SAELRKYADWGIMEKAKALKETPPNPT---KAAQIKADGHADVKGSDWGFGYQLAWMWDI
190 200 210 220 230

250 260 270 280 290 299
m989.pep NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKAMW-STMLAANGYTANEKARVKIVTPES
|||||
a989 NDRARVGVNYRSKVSHTLKGDAEWAADDAMAKQLWDANKLALLGYTPSEKARVKIVTPES

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1407

	240	250	260	270	280	290
m989.pep	300	310	320	330	340	350
	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAEVFEKEKTVVKGKSLRTTITPNWRNTYKV					
a989	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAEVFEKEKTVNGKSDRTTITPNWRNTYKV					
	300	310	320	330	340	350
m989.pep	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
a989	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
	360	370	380	390	400	410
m989.pep	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					
a989	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					
	420	430	440	450	460	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2991>:

```

m990.seq
1  ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCCTACCA AAATCGGCGA
51  CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTCCAG CGGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAATTACAAT AGCGGCATCC TCGCCGTCGA
201 TAATATGCCC GTTGTCAAAA AATATATTAC AGAGAAGTAT GGGGCTGATT
251 TAAAGCAGGC GGTAAAAAGT CAATTACAGG ATTTATACAA AACAAAGACCG
301 GAAGCTTGGG CAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGCACA
351 GTTTGGAACA AAATTTAGTA CGCTCAAACA GACGATGCCC GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCCAC GTCGCCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TAGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAAGTAC
651 CGTCCATAAG GATTATGCGG GCGCGCGGGA TTTCTGTTC GGCTACGACG
701 TGCGGGAGTC GGACGAACCC GCCCTGACCT TTGAAGACAA AGTCAGCGGA
751 CAATCCGGCG TGGTTTGGGA ACGCCGGCCG GAAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CAAAAACGGC GGATTCCGGT TCGTTTGGCT
851 TTAAACAAAA TTACCGGCAG GACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCAAC AGGTTATGC GGCATAACT TTGTTTGGGC
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCGT
1051 CAAAAATTGT GGCTGCGCTT CATCGGCGGC CGGTGCGATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GGTGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GACTGGCAAT CGGCGTGATG
1201 GCGGCGAGGG CCGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTGAT TTGTATGGTT ATGGCGGGGG TGTATTGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCGG AACGCTACAA
1401 AACCAAAGGT TGGACGGCTT CTGTGGAAGG CGGCTACAAC GCGCTTGTGG
1451 CGGAAGGCAT TGTGCGAAAA GGCAATAATG TGGCGTTTTA CCTACAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGCGCGG TCAGTGGCAA AGCCGCGCGG
1601 GCATTGCGGC AAAAAACCGT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGGCG CTTTTAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCA CTCGAAGGGC
1751 GGTTCGGTAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TATGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
1851 GCTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2992; ORF 990>:

m990.pep

1408

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGKNYN SGILAVDNMP VVKYITEKY GADLKQAVKS QLQDLYKTRP
101 EAWAENKKRT EEAYIAQFGT KFSTLTKQTMP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK DYAGGADFLF GYDVRESDEP ALTFEDKVSQ
251 QSGVVLERRP ENLKTLDGRK LIAAKTADSG SFAPKQNYRQ GLYELLKQK
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGWRKGVQ IGGEVFVRQN EGSRLAIGVM
401 GGRAGQHASV NGKGGAGSD LYGYGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGIVGK GNNVRFYLQP
501 QAQFTYLVGN GGFTDSEGTA VGLLGSGWQ SRAGIRAKTR FALRNGVNLQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LCRFGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSSLWLF*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2993>:

a990.seq

```

1 ATGTTCCAGAG CTCAGCTTGG TTCAAATACT CGTTCACCA AAATCGGCCGA
51 CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTCCAG CGGTAAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AACTACAAT AGCGGCATAC TCGCCGTCGA
201 TAATATGCCC GTTGTTAAGA AATATATTAC AGATACTTAC GGGGATAATT
251 TAAAGGATGC GGTAAAGAAG CAATTACAGG ATTTATACAA AACAGACCC
301 GAAGCTTGGG AAAAAATAA AAAACGGACT GAGGAGGCGT ATATAGAACA
351 GCTTGGACCA AAATTTAGTA TACTCAAACA GAAAAACCCC GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCCAC GTCGCCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TATGCTGGAA
601 ACTTCGGATA ATGCCCGCAT CCGCTGAAC ACGAAAGATG AAAAAACTGAC
651 CGTCCATAAA GCGTATCAGG GCGGTGCGGA TTTCTGTTC GGCTACGACG
701 TGCGGGAGTC GGACAAACCC GCCCTGACCT TTGAAGAAAA AGTCAGCGGA
751 CAATCCGGCG TGGTTTGGGA ACGCCGCCG GAAATCTGA AACGCTCGA
801 CGGGCGCAA CTGATTGCGG CGGAAAGGC AGACTCTAAT TCGTTTGCCT
851 TTAAACAAAA TTACCGGCAG GACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCAAC AGGCTTATGC GGCAATACT TTGTTGGGC
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCCGCGA TCCGTCCCCT
1051 CAAAAATTGT GGCTGCGCTT CATCGGCGGC CGGTGCGATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GCGGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTGT ACGGCAAAAT GAAGGCAGCC GGCTGGCAAT CGGCGTGATG
1201 GCGGCGAGG CTGGCCAGCA CGCATCAGT AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTTAT TTGCATGTT ATGGCGGGG TGTATTGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACGCAT CAATGATGAA AACCGTGCGG AACGCTACAA
1401 AACCAAGGT TGGACGGCTT CTGTGGAAG CCGCTACAAC GCGCTGTGG
1451 CGGAAGGCGT TGTCGGAAAA GGCAATAATG TGCGGTTTTA CCTGCAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAGTGCAA AGCCGCGCCG
1601 GCATTCGGGC AAAAAACCCGT TTTGCTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGCCG CTTTTAATGT TTTGCACAGG TCAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCG CTCGAAGGGC
1751 GGTTCCGCAT TGAAGCCGT TGGAAAGGCC ATATGTCCG ACGCATCGGA
1801 TACGGCAAAA GGACGGACGG CGACAAAGAA GCCGATTGT CGCTCAATG
1851 GCTGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2994; ORF 990.a>:

a990.pep

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGKNYN SGILAVDNMP VVKYITDTY GDNLKDAVKK QLQDLYKTRP
101 EAWAENKKRT EEAYIEQLGP KF---LKQKNP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHMLE
201 TSDNARIRLN TKDEKLTVHK AYQGGADFLF GYDVRESDEP ALTFEEKVSG
251 QSGVVLERRP ENLKTLDGRK LIAAEKADSN SFAPKQNYRQ GLYELLKQK
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGRRKGVQ IGGEVFVRQN EGSRLAIGVM

```

1409

401 GGRAGQHASV NGKGGAA~~SSY~~ LHGYGGGVYA AWHQLRDKQT GAYLDGWLQY
 451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGVVGK GNNVRFYLPQ
 501 QAQFTYLGVN GGFTDSEGTA VGLLGGSQWQ SRAGIRAKTR FALRNGVNLQ
 551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
 601 YGKRTDGDKE AALSLK~~WLF~~*

m990/a990 96.0% identity in 619 aa overlap

	10	20	30	40	50	60
m990.pep	MFR	Q	L	G	S	N
a990	MFR	Q	L	G	S	N
	70	80	90	100	110	120
m990.pep	S	G	I	L	A	V
a990	S	G	I	L	A	V
	130	140	150	160	170	180
m990.pep	K	F	S	T	L	K
a990	K	F	S	T	L	K
	190	200	210	220	230	240
m990.pep	M	T	L	K	D	S
a990	M	T	L	K	D	S
	250	260	270	280	290	300
m990.pep	A	L	T	F	E	K
a990	A	L	T	F	E	K
	310	320	330	340	350	360
m990.pep	E	G	G	F	C	L
a990	E	G	G	F	C	L
	370	380	390	400	410	420
m990.pep	R	S	H	Q	N	I
a990	R	S	H	Q	N	I
	430	440	450	460	470	480
m990.pep	L	H	G	Y	G	G
a990	L	H	G	Y	G	G
	490	500	510	520	530	540
m990.pep	A	L	V	A	E	G
a990	A	L	V	A	E	G
	550	560	570	580	590	600
m990.pep	F	A	L	R	N	G
a990	F	A	L	R	N	G

1410

	550	560	570	580	590	600
	610	620				
m990.pep	YGKRTDGDKEAALSLKWLFX					
a990	YGKRTDGDKEAALSLKWLFX					
	610	620				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2995>:

g992.seq

```

1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCC  TGTCGCTTTT  GGGCGCGTTG  GGTATACGG
101 GATATGACAG  TGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GGCACGTGAG  GGGACGTGGG  TTTCGACGCG  CCGTTTCGCC  GACGGGCATC
201 GCGGAAATCC  GGCCACAGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGATACCCT  TCACGTCATC  GACGCGCAGC  GCGCGAAACA  TAAATTCGG
301 ATGGCGTATA  TCGACGCACC  GGAGATGAAA  CAGGCTTACG  GTACAGTTC
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAGGG  TAGGAAAGTC  TTGTACGTG
401 TGTTTGAAAC  CGACCGCTAT  CAGCGCGAAG  TGGCGCAGGT  ATCCGCCGGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGCGCG  CGTGGCATTG
501 TAAAAGTTAT  GCTAAAGAAC  AGCAGGATAA  GCGCGATTTT  GCCGACTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAATCCGC  AAGCGCCGTG  GCGGTACCGC  CGGCGAGGCA  GGAGCGGCGG
651 GGGCAATAAG  GATTGGATGG  ATTCGTGGG  CGAATGGTTG  GGCATTGGT
701  AA

```

This corresponds to the amino acid sequence <SEQ ID 2996 ORF 992.ng>:

g992.pep

```

1  MFRHRHLKN  MQIKKIMKWL  PVALSLLGAL  GYTGVDSEAV  RTAVAVLDVL
51  GTAGDVGFDA  PVRRRASAKS  GHSYTGTVSK  VYDGDTLHVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFETDRY  QREVAQVSAG
151 KTDNLNMQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWMDSVGEWL  GIW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2997>:

m992.seq

```

1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCC  TGTCGCTTTT  GGGTGCCTTG  GGTATACGG
101 GGTACGGCAG  CGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GGGCGGGCAG  GGGACGCGGG  TTCCGACGCG  CCGGCCCGCC  GCCGAGCATC
201 GCGGAAATCC  GGCCACCGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGACACCCT  TCACGTTATC  GACGGCGACG  GCGCGAAACA  CAAAATCCGG
301 ATGGCGTATA  TCGACGCGCC  GGAGATGAAA  CAGGCTTACG  GCACGCGTTC
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAAGG  CAGGAAAGTC  AGCGTSCGCG
401 TGTTTCGATC  CGACCGCTAC  CAGCGCGAAG  TGGCGCAGGT  TTCTGTCGGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGCGCG  CGTGGCATTG
501 TAAAAGTTAT  GCTAAAGAAC  AGCAGGATAA  GCGCGATTTT  GCCGATTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAATCCGC  AAGCGCCGTG  GCGGTACCGC  CGAGCAGGCA  GGAGCGGCGG
651 GGGCAATAAG  GATTGGATGG  ATGCCGTGGG  CGAATGGTTG  GGCATTTGGT
701  AA

```

This corresponds to the amino acid sequence <SEQ ID 2998; ORF 992>:

m992.pep

```

1  MFRHRHLKN  MQIKKIMKWL  PVALSLLGAL  GYTGYGSEAV  RTAVAVLDVL
51  GAAGDAGSDA  PARRRASAKS  GHRYTGTVSK  VYDGDTLHVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFDTDRY  QREVAQVSVG
151 KTDNLNMQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWMDAVGEWL  GIW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 992 shows 96.1% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. gonorrhoeae*

m992/g992 96.1% identity in 233 aa overlap

1411

	10	20	30	40	50	60
m992.pep	MFRHRHRLKNNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDV LGAAGDAGSDA					
g992	MFRHRHRLKNNMQIKKIMKWL PVALSLLGALGYTGYDSEAVRTAVAVLDV LGTAGDVGFDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m992.pep	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
g992	PVRRRASAKSGHSYTGTVSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m992.pep	LRAAAEGRKVSVRVFD TDRYQREVAQVS VGKTD LNLMOVQDGA AWHYKSYAKEQQDKADF					
g992	LRAAAEGRKVSVRVFET DRYQREVAOVS AGKTD LNLMOVQDGA AWHYKSYAKEQQDKADF					
	130	140	150	160	170	180
	190	200	210	220	230	
m992.pep	ADYADAQIQAEERERKGLWKA KNPQAPWAYRRAGRSGG GKNKDWMDAVGEWLGIW*					
g992	ADYADAQIQAEERERKGLWKA KNPQAPWAYRRAGRSGG GKNKDWMDSVGEWLGIW*					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2999>:

a992.seq

```

1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCT  TGTCGCTTTT  GGGTGCGTTG  GGTATACGG
101 GGTACGGCAG  CGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GGC GCGGCAG  GGGACGCGGG  TTCCGACGCG  CCCGCCCGCC  GCCGAGCATC
201 GGC GAAATCC  GGCCACCGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGACACCC  TCACGTTATC  GACGGCGACG  GCGCGAAACA  CAAATCCGG
301 ATGGCGTATA  TCGACGCGCC  GGAGATGAAA  CAGGCTTACG  GCACGCGTTC
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAAGG  CAGGAAAGTC  AGCGTCCGCG
401 TGTTTCGAC  CGACCGCTAC  CAGTCCGAAC  TGGTCTTAGG  TTCTGTCCGC
451 AAAACCGAT  TGAACCTGAT  GCAGGTGCAG  GACGGGGCGG  CGTGGCATT
501 TAAAGTTAT  GCTAAAGAAC  AGCAGGATAA  GGCGGATTTT  GCCGATTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAATCCG  AAGCGCCGTG  GCGTACCGC  CGGGCAGGCA  GGAGCGGCGG
651 GGGCAATAAG  GATTGGATGG  ATGCCGTGGG  CGAATGGTTG  GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 3000; ORF 992.a>:

a992.pep

```

1  MFRHRHRLKN  MQIKKIMKWL  PVALSLLGAL  GYTGYGSEAV  RTAVAVLDVL
51  GAAGDAGSDA  PARRRASAKS  GHRYTGTVSK  VYDGD TLHVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFDTDRY  QREVAQVSVG
151 KTD LNLMOVQ  DGA AWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGG GKN  KDWMDAVGEWL  GIW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 992 shows 100.0% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. meningitidis*

a992/m992 100.0% identity in 233 aa overlap

	10	20	30	40	50	60
a992.pep	MFRHRHRLKNNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDV LGAAGDAGSDA					
m992	MFRHRHRLKNNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDV LGAAGDAGSDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a992.pep	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
m992	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
	130	140	150	160	170	180

1412

```

a992.pep      LRAAAEGRKVSVRVFDTRYQREVAQVSVGKTDNLNQVQDGAAWHTKSYAKEQQDKADF
               |||
m992          LRAAAEGRKVSVRVFDTRYQREVAQVSVGKTDNLNQVQDGAAWHYKSYAKEQQDKADF
               |||
               130      140      150      160      170      180

a992.pep      ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGKNKDWMDAVGEWLGIX
               |||
m992          ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGKNKDWMDAVGEWLGIX
               |||
               190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3001>:

```

g993.seq
1   CTGAAAGTCG TATTGGGCAG TTTTCAAGGC CCTTTGGATC TGCTGCTCTA
51  CCTTATCCGC AAGCAGAACA TCGATGTTCT CGATATTCCG ATGGTGGAAG
101 TTACCGGGCA GTATCTGCAC TATATTGCC AAATGGAAGC CTATCAGTTT
151 GATTTGCGCG CGGAATATCT TTTGATGGCG GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAGGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCGCTCTGC TTGCCTACGA GCAATGAAA
301 CTGGCGGCGC AGGGTTTGA CGCGCTGCCG CGTGGCGGAC GGGATTTCGC
351 GTGGGCTTAC CTGCCGCTGG AAATTGCAGC CGAGACGAAG CTGCCCGAGG
401 TTTACATCGC CGATTTGATG CAGGCATGGT TGGGCATTCT TTCTCGGGCA
451 AAACATACGC GCAGCCACGA AGTAATCAA GAAACCTTT CCGTGCGCGC
501 GCAAATGACG GCAATCCTGC GCCGTTTGAA CGAACACGGG ATATGCAGGT
551 TTCACGCCCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GATCGTCAAC
601 TTCATCGCCC TGTGGAGCT TGCCAAAGAA GGATTGGTCG GAATCGTACA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTCGGC ACACGGGGCG GCGCGATGT CTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3002 ORF 993.ng>:

```

g993.pep
1   LKVVLSFGQ PLDLLLYLIR KQNIQVLDIP MVEITGQYLH YIAQMEAYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTAEVED EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAAETK LPEVYIADLM QAWLGILSRA
151 KHTRSHEVIQ ETLSVRAQMT AILRRLNEHG ICRFHALFNP EQGAAYVIVN
201 FIALLELAKE GLVRIVQEDG FGEIRISLNH EGAHSDGIFG TRGGRDVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3003>:

```

m993.seq
1   TTGAAAGTCG TATTGGGCAG CTTCGAAGGC CCTTTGGATC TACTGCTGTA
51  TCTGATCCGC AAACAGAATA TCGACGTACT GGATATTCCG ATGGTGAAGA
101 TTACCGAGCA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
151 GATTTGCGCG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAAC CGTCGAAGAC GAAGAAGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCTTGC TGGCTTACGA ACAGATGAAG
301 CTGGCGGCGC AGGGTTTGA CGCGCTGCCG CGAGCCGGAC GGGATTTCGC
351 GTGGGCTTAC CTGCCGCTGG AAATTGCCGT CGAAGCCAAAG CTGCCCGAAG
401 TCTATATTAC CGACTTGACG CAAGCGTGGC TGGGTATTTT GTCTCGGGCA
451 AAACACACGC GCAGCCACGA AGTAATCAA GAAACCATCT CCGTGCGCGC
501 GCAAATGACG GCAATCCTGC GCCGTTTGAA CGGACACGGA ATATGCAGGT
551 TTCACGACCT GTTCAATCCC AAACAGGGCG CGGCTTACGT GGTCTGCAAC
601 TTCATCGCAC TGTGGAGCT TGCCAAAGAA GGATTGGTCA GAATCGTGCA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTCGGC ACACGAGGCG GCGCGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3004; ORF 993>:

```

m993.pep
1   LKVVLSFGQ PLDLLLYLIR KQNIQVLDIP MKVITEQYLH YIAQIETYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTETVED EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLGILSRA
151 KHTRSHEVIK ETISVRAQMT AILRRLNNGH ICRFHDLFNP KQGAAYVVVN
201 FIALLELAKE GLVRIVQEDG FGEIRISLNH EGAHSDGISG TRGGRDVF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 993 shows 93.1% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. gonorrhoeae*

1413

m993/g993 93.1% identity in 248 aa overlap

m993.pep	10	20	30	40	50	60
	LKVVLSFGQPLDLLLYLRKQNI	DVLDIPMVKITEQYLHYIAQI	ETYQFDLAAEYLLMA			
g993	10	20	30	40	50	60
	LKVVLSFGQPLDLLLYLRKQNI	DVLDIPMVEITGQYLHYIAQME	AYQFDLAAEYLLMA			
m993.pep	70	80	90	100	110	120
	AMLIEIKSRLLLPRTETVEDEE	ADPRAELVRRLLAYEQMKLAAQ	GLDALPRAGRDFAWAY			
g993	70	80	90	100	110	120
	AMLIEIKSRLLLPRTAEVEDEE	ADPRAELVRRLLAYEQMKLAAQ	GLDALPRAGRDFAWAY			
m993.pep	130	140	150	160	170	180
	LPLEIAVEAKLPEVYITDLTQ	AWLGILSRAKHTRSHEVIKETI	SVRAQMTAILRRLNKG			
g993	130	140	150	160	170	180
	LPLEIAAETKLPEVYIADLMQ	AWLGILSRAKHTRSHEVIQETL	SVRAQMTAILRRLNKG			
m993.pep	190	200	210	220	230	240
	ICRFHDLFNPQGAAYVVVNFIA	LLELAKEGLVRIVQEDGFGEIR	ISLNHEGAHSDGISG			
g993	190	200	210	220	230	240
	ICRFHDLFNPQGAAYVIVNFIA	LLELAKEGLVGIVQEDGFGEIR	ISLNHEGAHSDGIFG			
m993.pep	249					
	TRGGRDVF					
g993	249					
	TRGGRDVF					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3005>:

a993.seq

1	CTGAAAGTCG	TATTGAGCAG	TTTCAAGGC	CCTTTGGATC	TGCTGCTCTA
51	CCTTATCCGC	AAGCAGAACA	TCGATGTTCT	CGATATTCCG	ATGGTGAAGA
101	TTACCGAACA	GTATCTGCAC	TACATCGCCC	AAATAGAAAC	CTATCAGTTT
151	GATTTGGCGG	CGGAATATCT	TTTGATGGCA	GCAATGCTGA	TTGAAATCAA
201	ATCGCGCCTG	CTGCTGCCGC	GTACCGAAAC	CGTCGAAGAC	GAAGAAGCCG
251	ACCGCGGTGC	CGAGTTGGTG	CGCCGCCTGC	TGGCTTACGA	GCAGATGAAG
301	CTGGCGGCAC	AAGGTTTGGG	TGCGCTTCCT	CGTGCGGGCC	GGGATTTGCG
351	ATGGGCATAC	CTGCCACTGG	AAATTGCCGT	CGAAGCCGAG	CTGCCCGAAG
401	TCTATATTAC	CGACTTGACG	CAGGCGTGGC	TGAGTATTTT	GTCTCGGGCA
451	AAACATACGC	GCAGCCACGA	AGTTATCAAA	GAAACCATCT	CCGTGCGCGC
501	GCAAATGACG	GCAATCCTGC	GCCGTTTGAA	CAAACACGGG	ATATGCAGGT
551	TTACAGACCT	GTTCAATCCC	GAACAGGGCG	CGGCTTACGT	GGTCGTCAAC
601	TTATATCGAC	TGTTGGAGCT	TGCCAAAGAA	GGTTTGGTCG	GAATCGTACA
651	GGAAATCGGT	TTCGGAGAAA	TCCGAATCAG	CCTCAATCAT	GAGGGGGCGC
701	ATTCAGACGG	CATTTCGGGC	ACACGGGGCG	GGCGCGATGT	GTTCTAA

This corresponds to the amino acid sequence <SEQ ID 3006; ORF 993.a>:

a993.pep

1	LKVVLSFGQ	PLDLLLYLR	KQNI	DVLDIP	MVKITEQYLH	YIAQIETYQF
51	DLAAEYLLMA	AMLIEIKSR	LLPRTETVED	EEADPRAELV	RRLAYEQMK	
101	LAAQGLDALP	RAGRDFAWAY	LPLEIAVEAK	LPEVYITDLT	QAWLSILSRA	
151	KHTRSHEVIK	ETISVRAQMT	AILRRLNKHG	ICRFHDLFNP	EQGAAYVVVN	
201	FIALLELAKE	GLVGIVQEVG	FGEIRISLNH	EGAHSDGISG	TRGGRDVF*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 993 shows 97.6% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. meningitidis*

a993/m993 97.6% identity in 248 aa overlap

a993.pep	10	20	30	40	50	60
	LKVVLSFGQPLDLLLYLRKQNI	DVLDIPMVKITEQYLHYIAQI	ETYQFDLAAEYLLMA			
m993	10	20	30	40	50	60
	LKVVLSFGQPLDLLLYLRKQNI	DVLDIPMVKITEQYLHYIAQI	ETYQFDLAAEYLLMA			

1414

	10	20	30	40	50	60
a993.pep	70	80	90	100	110	120
	AMLEIEIKSRLLLPRTETVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPFRGRDFAWAY					
m993	70	80	90	100	110	120
	AMLEIEIKSRLLLPRTETVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPFRGRDFAWAY					
a993.pep	130	140	150	160	170	180
	LPLEIAVEAKLPEVYITDLTQAWLSILSRKHTRSHEVIKETISVRAQMTAILRRLNKHG					
m993	130	140	150	160	170	180
	LPLEIAVEAKLPEVYITDLTQAWLGILSRKHTRSHEVIKETISVRAQMTAILRRLNKHG					
a993.pep	190	200	210	220	230	240
	ICRFHDLFNPQGAAYVVVNFIALLELAKEGLVGVQEVGFGEIRISLNHEGAHSDGISG					
m993	190	200	210	220	230	240
	ICRFHDLFNPQGAAYVVVNFIALLELAKEGLVRIVQEDGFGFEIRISLNHEGAHSDGISG					
a993.pep	249					
	TRGGRDVF					
m993	TRGGRDVF					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3007>:

g996.seq

```

1 ATGAACAGAA GAACCTTCCT CCTCGGCGCA GGC GCGTTGC TTCTTACCGC
51 CTGCGGCAGAA AAATCCGCCG GAACCCACGC CAAAATTCCC GAAGGAAGCA
101 CCGTGCTTGC CTTGGGCGAT TCGCTACCT TCGGCTACGG AGCAAACCCG
151 GGCGAATCCT ACCCGCGCA ACTGCAAAAA CTGACGGGTT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACGTCCGC GCAAGCCCTA TCGCGCTGC
251 CCGCGCTGTT GGCACGCAAA CCCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TCGCAAAAGT TCCCGAGGAG CAGACCCGCG CCAATATCGC
351 GAAAATCATC GAAACCGTGC AAAAGGAAAA CATCCCGGCC GTCTCGTCG
401 GCGTGCCGCA CATCACA CTG GCGCGTTGT TCGGCGATT GAGCGACCAT
451 CCGCTGTATG AGGATTTGTC CGAGGAATAC GGCATTCCGT TGTTCGGCGG
501 CCGCTGGGCG GAAATTTTGG GCAATAATA TCTGAAATCC GACCAAATCC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTTC CCGAAATTT GAATCAATTT
601 TTGAGAAAAC ATGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3008 ORF 996.ng>:

g996.pep

```

1 MNRRTFLLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51 GESYPALQKQ LTGWNIVNGG VSGDTSAQAL SRLPALLARK PKLVIVIGG
101 NDFLRKVPPE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSHD
151 PLYEDLSEY GIPLFGGAWA EILGNLNLKS DOIHANGKGY RKFAENLNQF
201 LRKHGFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3009>:

m996.seq

```

1 ATGAACAGAA GAACCTTCCT CCTCGGCGCA GGC GCGTTGC TGCTTACCGC
51 CTGCGGCAGAA AAATCCGCCG GAACCCACGC CAAAATTCCC GAAGGAAGCA
101 CCGTACTTGC CTTGGGCGAT TCGCTTACCT TCGGCTACGG CGCAAACCCG
151 GGCGAATCCT ACCCGCGCA ACTGCAAAAA CTGACGGGTT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACATCTGC CCAAGCCCTG TCGCGCTGC
251 CCGCGCTGTT GGCACGCAAA CCCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TCGCAAAAGT TCCCAAGGAG CAGACCCGCG CCAATATCGC
351 GAAAATCATC GAAACCGTGC AGAAGGAAAA CATCCCGGCC GTCTCGTCG
401 GCGTGCCGCA CATCACA CTG GGTGCGTTGT TCGGCGATT GAGCGATCAT
451 CCGCTGTATG AGGATTTGTC CGAGGAATAC GGCATTCCGC TGTTCGGCGG
501 CCGCTGGGCG GAAATTTTGG GCGATAATA TCTGAAATCC GACCAAATCC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTTC CCGAAGATT GAATCAATTT
601 TTGAGAAAAC AGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3010; ORF 996>:

m996.pep

```

1 MNRRTFLLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51 GESYPALQKQ LTGWNIVNGG VSGDTSAQAL SRLPALLARK PKLVIVIGG

```

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```

101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH
151 PLYEDLSEY GIPFGGAWA EILGDNNLKS DQIHANGKY RKFAEDLNQF
201 LRKQGR

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 996 shows 98.1% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. gonorrhoeae*

```

m996/g996    98.1% identity in 207 aa overlap

      10      20      30      40      50      60
m996.pep    MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPAQLQK
          |||
g996         MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPAQLQK
          |||
      10      20      30      40      50      60

      70      80      90     100     110     120
m996.pep    LTGWNIVNGGVSGD TSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
          |||
g996         LTGWNIVNGGVSGD TSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
          |||
      70      80      90     100     110     120

      130     140     150     160     170     180
m996.pep    ETVQKENIPAVLVGVPHITL GALFGHLSDHPLYEDLSEY GIPFGGAWAEILGDNNLKS
          |||
g996         ETVQKENIPAVLVGVPHITL GALFGHLSDHPLYEDLSEY GIPFGGAWAEILGDNNLKS
          |||
      130     140     150     160     170     180

      190     200
m996.pep    DQIHANGKGYRKFAEDLNQFLRKQGR
          |||
g996         DQIHANGKGYRKFAEDLNQFLRKQGR
          |||
      190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3011>:

```

a996.seq
1  ATGAACAGAA GAACCTTCCT CCTCGGCGCA GGCGCGTTGC TCCTTACCGC
51 CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAAATTCCC GAAGGAAGCA
101 CCGTACTTGC CTTGGGCGAT TCGCTTACCT TCGGCTACGG CGCAAACCCC
151 GGCGAATCCT ACCCGCGCA ACTGCAAAAA CTGACGGGTT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACATCCGC CCAAGCCCTG TCGCGCCTGC
251 CCGCGCTGTT GGCACGCAA CCAAGCTTG TGATTGTCGG CATAGCGCGC
301 AACGACTTTC TCGCAAAAGT TCCCAAGGAG CAGACCCGCG CCAATATCGC
351 GAAAATCATC GAAACCGTGC AGAAGGAAAA CATCCCGGCC GTCCTCGTCG
401 GCGTGCCGCA CATTACCTTG GCGCGTTGT TCGGGCATTT GAGCGATCAT
451 CCGCTGTATG AGGATTGTG CGAGGAATAC GGCATTCCGC TGTTCGGCGG
501 CCGGTGGGCG GAAATTTTGG GCGATAATAA TCTGAAATCC GACCAATCC
551 ACGCCAACGG CAAAGCTAT CGGAAATTTG CCGAAGATTT GAATCAATTT
601 TTGAGAAAAC AGGGGTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3012; ORF 996.a>:

```

a996.pep
1  MNRRTFLLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51 GESYPAQLQK LTGWNIVNGG VSGD TSAQAL SRLPALLARK PKLVIVGIGG
101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH
151 PLYEDLSEY GIPFGGAWA EILGDNNLKS DQIHANGKY RKFAEDLNQF
201 LRKQGR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 996 shows 100.0% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. meningitidis*

```

a996/m996    100.0% identity in 207 aa overlap

      10      20      30      40      50      60
a996.pep    MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPAQLQK

```

1416

```

|||||
m996      MNRRFTLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPAQLQK
          10      20      30      40      50      60

          70      80      90      100     110     120
a996.pep  LTGWNIVNGGVSGDTSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
          70      80      90      100     110     120
m996      LTGWNIVNGGVSGDTSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
          70      80      90      100     110     120

          130     140     150     160     170     180
a996.pep  ETVQKENIPAVLVGVPHITLGALFGHLSHDHPLYEDLSEYGIPLFGGAWAEILGDNNLKS
          130     140     150     160     170     180
m996      ETVQKENIPAVLVGVPHITLGALFGHLSHDHPLYEDLSEYGIPLFGGAWAEILGDNNLKS
          130     140     150     160     170     180

          190     200
a996.pep  DQIHANGKGYRKFAEDLNQFLRKQGFRR
          190     200
m996      DQIHANGKGYRKFAEDLNQFLRKQGFRR
          190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3013>:

```

g997.seq (partial)
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51 CTGGGCCGGC TTGTCCGCCG CCGTCACCTT GCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GAAGGGCGCG CACACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGCGGTGT TGC GCCTGAT GAAACCATC GGTTCAGACC
251 CCCGTGCCGC CTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCGCCCGCG CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGCGCGT TACCGTCCGC ATTCAAAGCC AAAGTCTTG
401 CCGATATGTC CGATTGTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTTGCAC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTGG CAGCCCTTGG TCTGGGCGCG GCTCAACACG CCTTTGGAAG
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCGACGCG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCGGAA CCCGCTTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAGC GCGCGTATGC CGTCTGAACA CCCTCCCGGA CGGAAAAGTC
751 CTCGTCAACG GCGAAGCCTT CGATGCCGCC ATACTTGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCTGCG CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGcCTGc CGCCCGCGTG AcCGCAttg CCGAcggcAC
951 ggcaCaatg CTGCTTTgcc cggGGCAGGC tccggactgc CcccaaAacg
1001 aagTCTCCGC cGTCAAttgc GTTTCGAcc GCGtcggcgC Gtttgcaaac
1051 cga...

```

This corresponds to the amino acid sequence <SEQ ID 3014 ORF 997.ng>:

```

g997.pep (partial)
1  MNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51 GNTDGFGLD NGQHILLGAY RGVLRIMKTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPSAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSDGVL
201 KKSQSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA ILATAPYHAA ALLPEGTPFH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGIADGTAQW LLC PGQAPDC PQNEVSAVIS VSDRVGAFAN
351 R...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3015>:

```

m997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51 CTGGGCCAGG CTGTCCGCCG CCGTCACCTT GCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GCAGGGCGCG CACACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGCGGTGT TGC GCCTGAT GAAACCATC GGTTCGGATC
251 CCCGTGCCGC CTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCGCCCGCG CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGCGGTG CACCGACTGC ATTCAAAGCC AAAGTCTTG
401 CCGATATGTC CGATTGTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTGAT
501 GCAGTTTGG CAGCCCTTGG TTTGGGCGCG GCTCAACACG CCTTTGGAAG

```

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```

551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAGCAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCGCCTTGG CGGATCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCCTCCCGGA CGGGAAAGTG
751 CTGCTCAACG GCGAAGCTTT CGATGCCGCC GTCCCGGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTGCTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGCTGACC CGCCCGCTG ACCGGCCTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGCAGGCT CGGACTGCCT GAAAACGAAG
1001 TGTCCGCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGGCGG ACAAAGCCCA CGCCGACCTC AAACGCATCC TTCCGCATTT
1101 GGGCGAACCC GAAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCGCCGCCG GACTTGTCGT GGTGACCG GCACCGCATC
1201 TTCCCGCGCG GCGACTACCT CCACCGGAC TACCCGCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 3016; ORF 997>:

```

m997.pep
  1 MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
  51 GNTDGFGLD NGQHILLGAY RGVRLRMKTI GSDPRAAFRL VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRAPTAFKA KLLADMSDLQ KSARLGQPD
151 TVAOWLKQRN VPRAAVMOFW QPLVWGALNT PLETASLRVL CNVLSGVL
201 KKSGSDYLLP KQDLGAIVAE PALADLQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLR
301 AEPVRLPAPL TGLADGTQVQW LLCRGRLGLP ENEVSAVISV SDRVGAFANR
351 AWADKAHADL KRILPHLGEP EAVRVITEKR ATTAADAPPP DLSWLHRHRI
401 FPAGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 997 shows 96.0% identity over a 351 aa overlap with a predicted ORF (ORF 997) from *N. gonorrhoeae*

g997/m997 96.0% identity in 351 aa overlap

g997.pep	10	20	30	40	50	60
m997	10	20	30	40	50	60
g997.pep	70	80	90	100	110	120
m997	70	80	90	100	110	120
g997.pep	130	140	150	160	170	180
m997	130	140	150	160	170	180
g997.pep	190	200	210	220	230	240
m997	190	200	210	220	230	240
g997.pep	250	260	270	280	290	300
m997	250	260	270	280	290	300
g997.pep	310	320	330	340	350	
m997	310	320	330	340	350	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3017>:

```
a997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51  CTGGGCGCGC TTGTCCGCGC CCGTTACCTT GCGCGGCGAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GCAGGGCGCG CCGACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ATATTTTACT
201 CCGGCGCATAC CGGGGCGTGT TCGCCTGAT GAAAACCATC GGTTTCAGAC
251 CCCATGCCGC CTTTTTGGCG GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCCGCG CCCTGCATA TTTTGGGCGG
351 CGTGTGCTT GCCCGGCGCG TACCGTCCG ATTCAAAGCC AAACGTCTTG
401 CCGATATGTC CGATTTGCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCGTAAT
501 GCAGTTTGG CAGCCCTTGG TTTGGGGCGC GCTCAACACG CCTTTGAAA
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCGGAA CCCGCTTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCATATGC CGTCTGAACA CCTCCCGGA CGGAAAGTG
751 CTCGTCACG GCGAACCTTT CGATGCCGCC GTCCCGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCGAACAC GTTCAGACG
851 CATATCAAAA CCTTCGCTAT CACGCCATCA CCACCGCTA TCTGCGCTAT
901 GCCGAACCCG TCCGCTTGCC TGCCCGCTG ACGGACTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGCAGGCT CGGACTGCCT GAAAACGAAG
1001 TGTCCGCGCT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGCGCG ACAAGTTC ACGCGACCTC AAACGCATCC TTCCGCATTT
1101 GGGCGAACC GAAGCCGTGC GCGTCATCAC GAAAAACGC GCCACAACG
1151 CAGCCGATGC CCGCGCGCG GATTGTCTGT GGTGCAACG GCACCGCATC
1201 TTCCCGCGCG GCGACTACCT CCACCCAGAC TACCCGCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA
```

This corresponds to the amino acid sequence <SEQ ID 3018; ORF 997.a>:

```
a997.pep
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARALA
51  GNTDGFGLD NGQHILLGAY RGVLRMLMTI GSDPHAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPSAFKA KLLADMSDLO KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSDGVL
201 KKSQSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRIC RLNTLPDGKV
251 LVNGEPFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLR?
301 AEPVRLPAPL TGLADGTVQW LLCRGRLGLP ENEVSAVISV SDRVGAFANR
351 AWADKVHADL KRILPHLGEP EAVRVITEKR ATTAADAPPP DLSWLHRHRI
401 FPGADYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 997 shows 98.2% identity over a 437 aa overlap with a predicted ORF (ORF 997) from *N. meningitidis*

a997/m997 98.2% identity in 437 aa overlap

	10	20	30	40	50	60
a997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARALAGNTDGFGLD					
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
	10	20	30	40	50	60
	70	80	90	100	110	120
a997.pep	NGQHILLGAYRGVLRMLMTIGSDPHAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
m997	NGQHILLGAYRGVLRMLMTIGSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a997.pep	ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
m997	ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
	190	200	210	220	230	240
a997.pep	PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALAELQRLGADIRLETRIC					

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```

m997      PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALADLQRLGADIRLETRVC
           190      200      210      220      230      240

           250      260      270      280      290      300
a997.pep  RLNTLPDGKVLVNGEPFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY
           |||||
m997      RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY
           250      260      270      280      290      300

           310      320      330      340      350      360
a997.pep  AEPVRLPAPLTGLADGTVOWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKXHADL
           |||||
m997      AEPVRLPAPLTGLADGTVOWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKHAHDL
           310      320      330      340      350      360

           370      380      390      400      410      420
a997.pep  KRILPHLGEPEAVRVITEKRATTAADAPPPDLSWLHRRHRIFFAGDYLHPDYPATLEAAVQ
           |||||
m997      KRILPHLGEPEAVRVITEKRATTAADAPPPDLSWLHRRHRIFFAGDYLHPDYPATLEAAVQ
           370      380      390      400      410      420

           430
a997.pep  SGFASAEACLQSLSDAVX
           |||||
m997      SGFASAEACLQSLSDAVX
           430

```

g999.seq Not found yet

g999.pep Not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3019>:

```

m999.seq
1  ATGAATATGA AAAAAATTGAT TTCCGCAATT TGTGTTTCAA TTGTTTTATC
51  AGCCTGCAAC CAACAATCAA AAACGCTTCA AGCTTAAAGAA CCTGTCCAAA
101 GTATCCAGGC TGCTGATTGT ACCGCCCCAA TGGACATCAC AGTTGAACAA
151 TATCTCATCA ATTTGGAGCA AGCATTTAAA ACTCAGAACG TCTCAACAAA
201 AATCCATAAT AAAAAATATTG TCAAGACCGA TTGTGGTTAT GACCTTACTT
251 TGGTAATGGA TTTTGGGGCG ATTGCGCTCA AACTGGACGA GCAGCAAAAA
301 ATTAGAGCTA TCTCAGTAGG CTACATTTTA AAAACCGACG GAGAGAAAGG
351 ACAAATCTA GTCAATAATG CCATAAATGG ATTACACAGT ATTCAGGCAG
401 TTCTGTCTTT AACTACCACA GACAAATTGG GCGAATCGGA AGCAGGAAAA
451 CAACTTTTTA CAGCTTTAAC CGAAGTCGTC AAAGAATCCA ATCAGACAGG
501 AGCAACAGCG CAAAAAGACG TTCCGGCAGA TGGTATTTTA TATAGCGTTG
551 TTTTGAATAA AGAAACAAAC ACCATTGCAA TAATCGGCAG AAAACAACCC
601 TAA

```

This corresponds to the amino acid sequence <SEQ ID 3020; ORF 999>:

```

m999.pep
1  MNMKKLISAI CVSIVLSACN QSKTAQAE PVQSIQAADC TAPMDITVEQ
51  YLINLEQAFK TQNVSTKIHN KNIVKTDGCG DLTLMDFGA IALKLDEQOK
101 IRAISVGYIL KTDGEKGQNL VNNAINGLHS IQAVLSLTTT DKLGESEAGK
151 QLFTALTEVV KESNOTGATA QKDV PADGIL YSVVFEKETN TIAIIGRKQP

```

a999.seq Not found yet

a999.pep Not found yet

The foregoing examples are intended to illustrate but not to limit the invention.

CLAIMS

1. A protein comprising a fragment of an amino acid sequence from SEQ ID 2790 wherein said fragment comprises at least 7 amino acids from said sequence.
2. A protein comprising an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020.
3. A protein having 50% or greater homology to a protein according to claim 1.
4. A protein comprising a fragment of an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020, wherein said fragment comprises 7 or more consecutive amino acids from said sequence.
5. An antibody which binds to a protein according to any one of claims 1 to 3.
6. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.
7. A nucleic acid molecule according to claim 5, comprising a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019.
8. A nucleic acid molecule comprising a fragment of a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019, wherein said fragment comprises 10 or more consecutive nucleotides from said sequence.
9. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 5.
10. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 6.
11. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 7.
12. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.
13. A composition according to claim 11 being a vaccine composition or a diagnostic composition.
14. A composition according to claim 11 for use as a pharmaceutical.
15. The use of a composition according to claim 11 in the manufacture of a medicament for the treatment or prevention of infection due to Neisserial bacteria.

16. A composition comprising a protein of claim 1 wherein said composition is immunogenic.

17. A composition comprising a protein of claim 2 wherein said composition is immunogenic.

18. A composition comprising a protein of claim 3 wherein said composition is immunogenic.

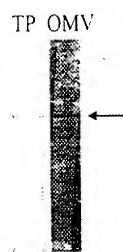
Fig. 2

279 (10.5 kDa)

A) PURIFICATION



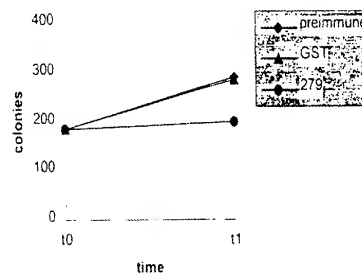
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY

E) ELISA assay: positive

279

The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that protein 279 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract, OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B)

Fig. 3

576 (27.8 kDa)

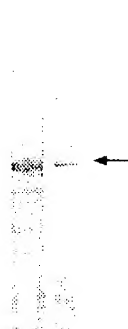
A) PURIFICATION

M1 576



B) WESTERN BLOT

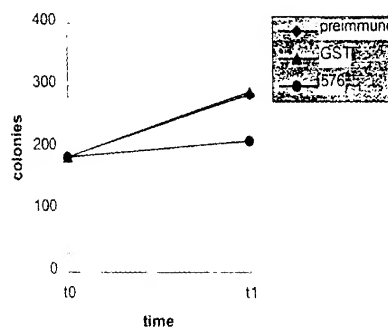
TP OMV



C) FACS



D) BACTERICIDAL ASSAY

E) ELISA assay: positive

576

The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 576 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 4

519 (33 kDa)

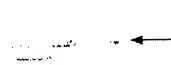
A) PURIFICATION

M1 519

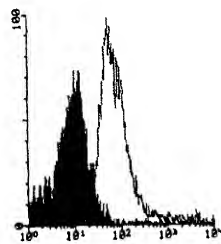


B) WESTERN BLOT

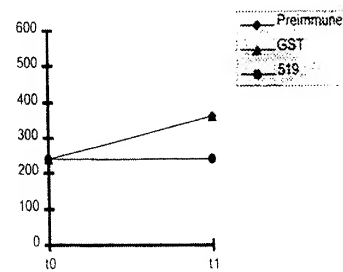
TP OMV



C) FACS



D) BACTERICIDAL ASSAY

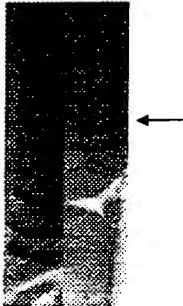
E) ELISA assay: positive

519

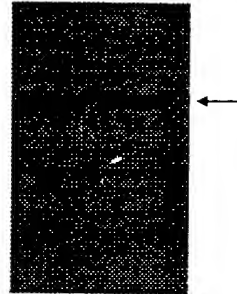
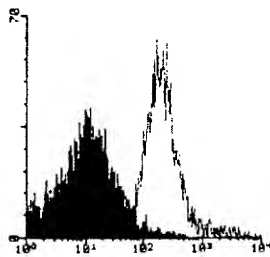
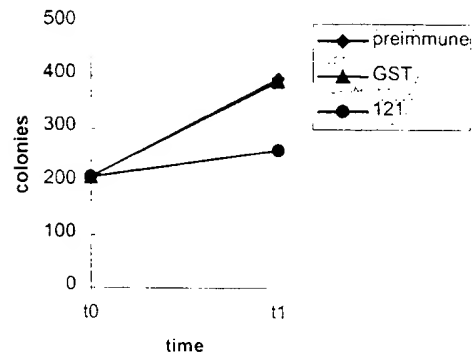
The predicted gene *519* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 519 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

121 (40 kDa)**A) PURIFICATION**

M1 121

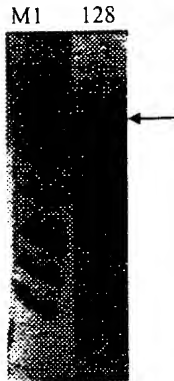
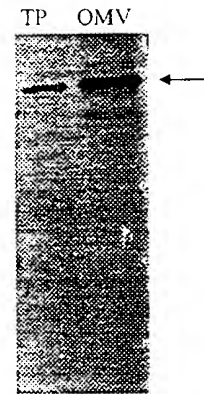
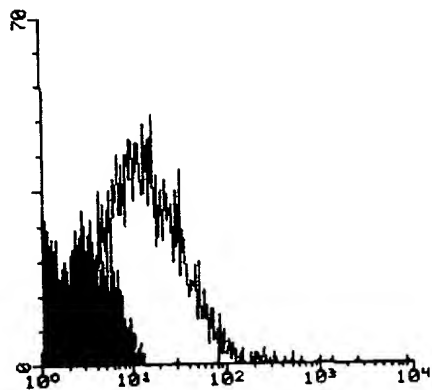
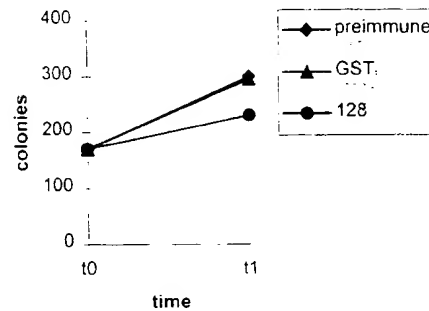
**B) WESTERN BLOT**

TP OMV

**C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****121**

The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

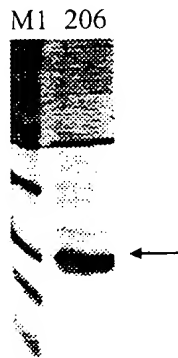
Fig. 5

128 (101 kDa)**Fig. 6****A) PURIFICATION****B) WESTERN BLOT****C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****128**

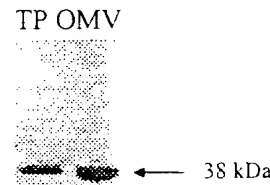
The predicted gene *128* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 7

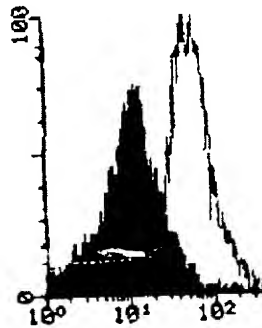
A) PURIFICATION



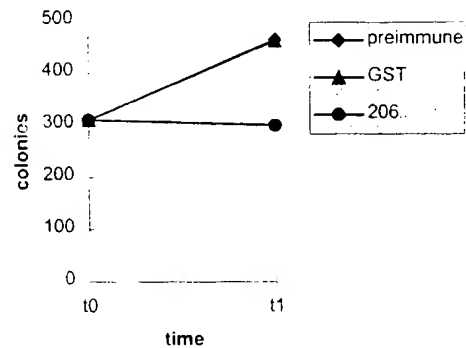
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY



E) ELISA assay: positive

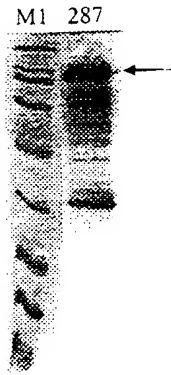
206

The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worth noting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a reactive band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C) is shown the FACS analysis, in panel D) the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

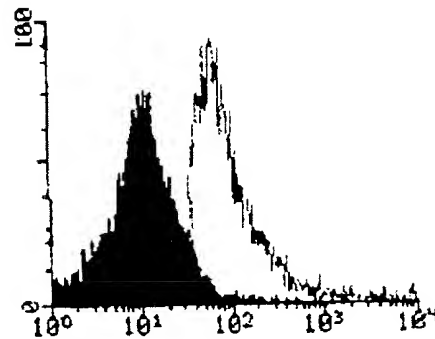
287 (78 kDa)

Fig. 8

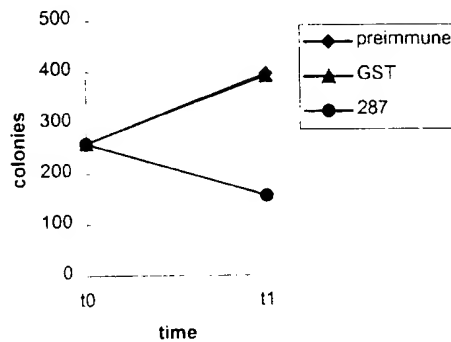
A) PURIFICATION



B) FACS



C) BACTERICIDAL ASSAY

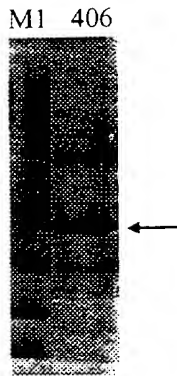
D) ELISA assay : positive**287**

The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A).

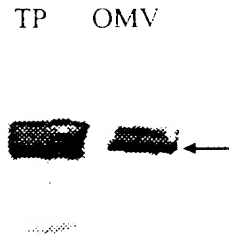
406 (33 kDa)

Fig. 9

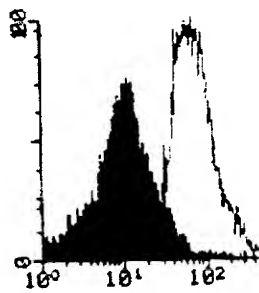
A) PURIFICATION



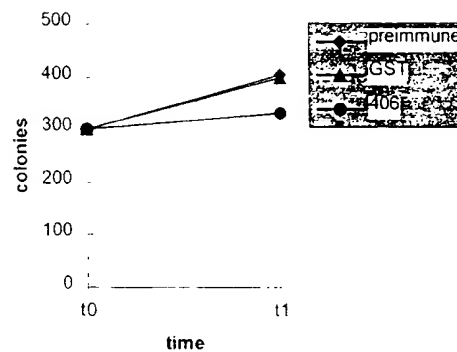
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY

E) ELISA assay : positive**406**

The predicted gene *406* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

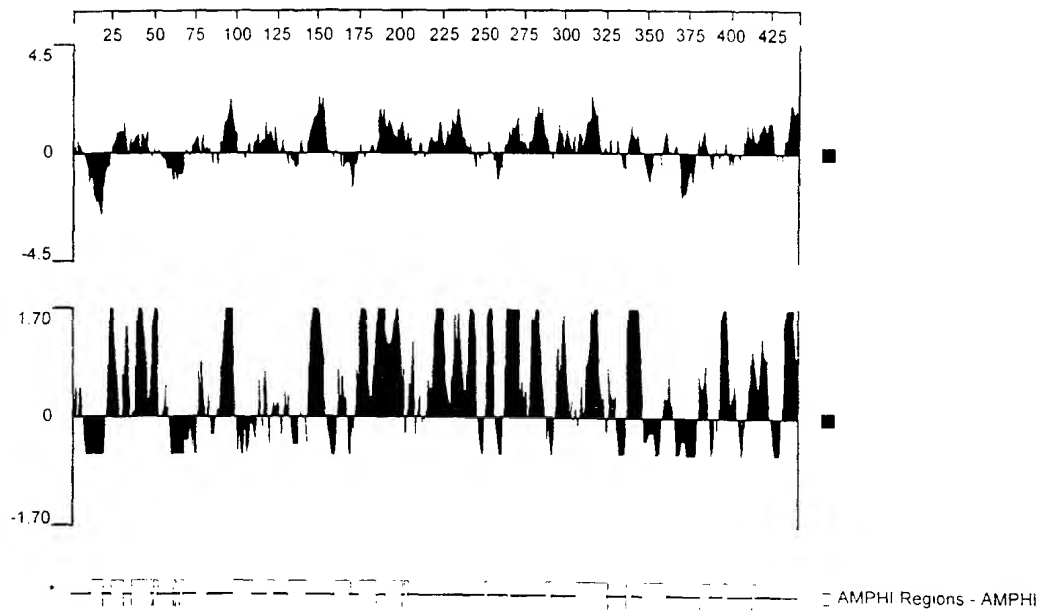
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 10

10/30

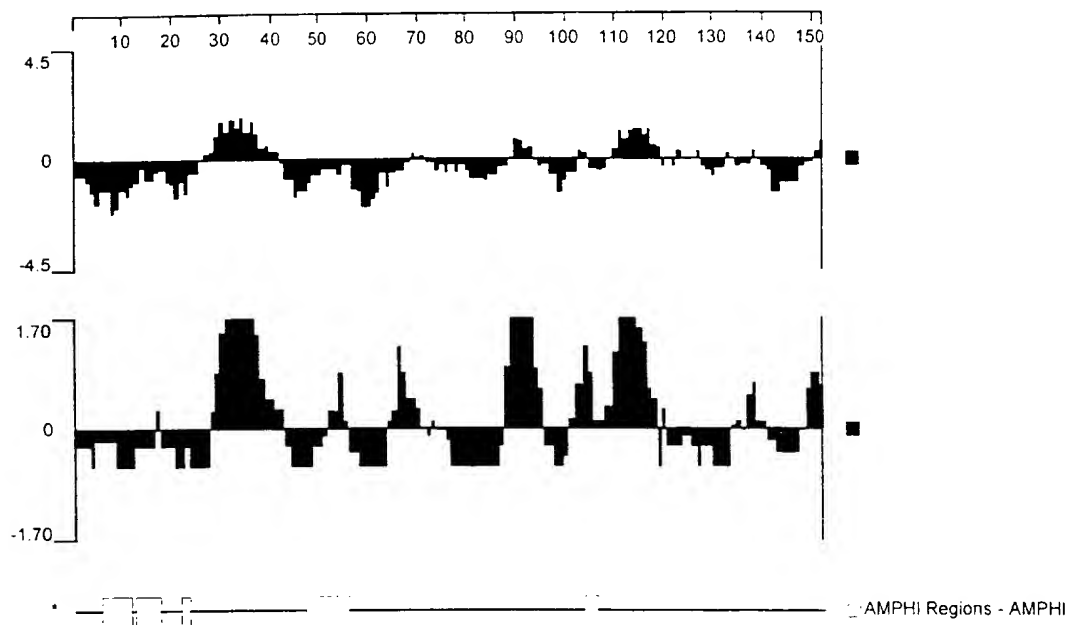
279Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 11

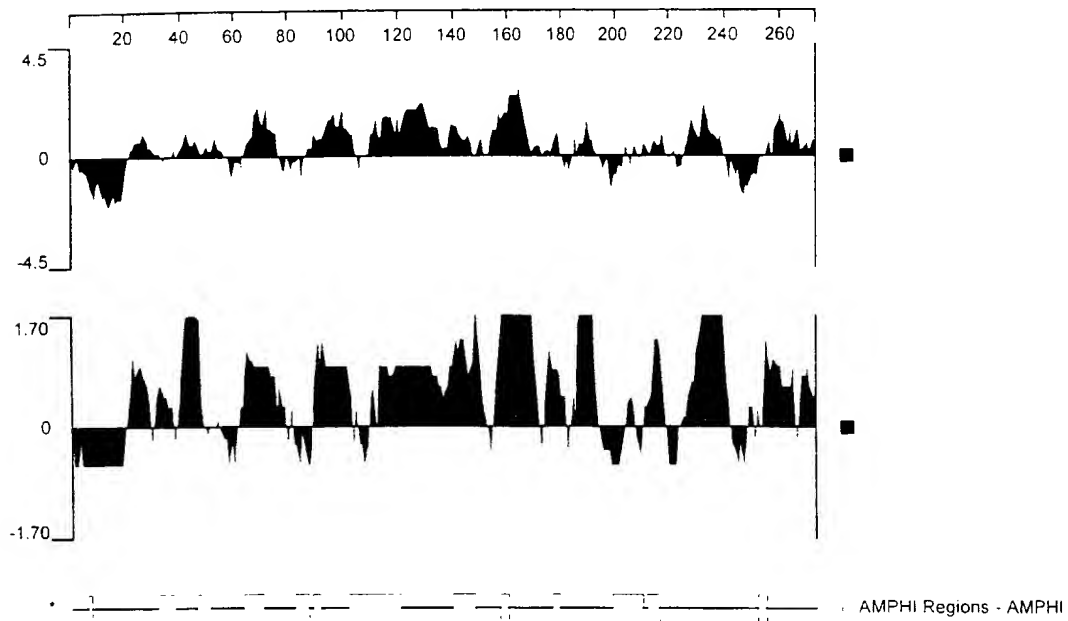
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 12

12/30

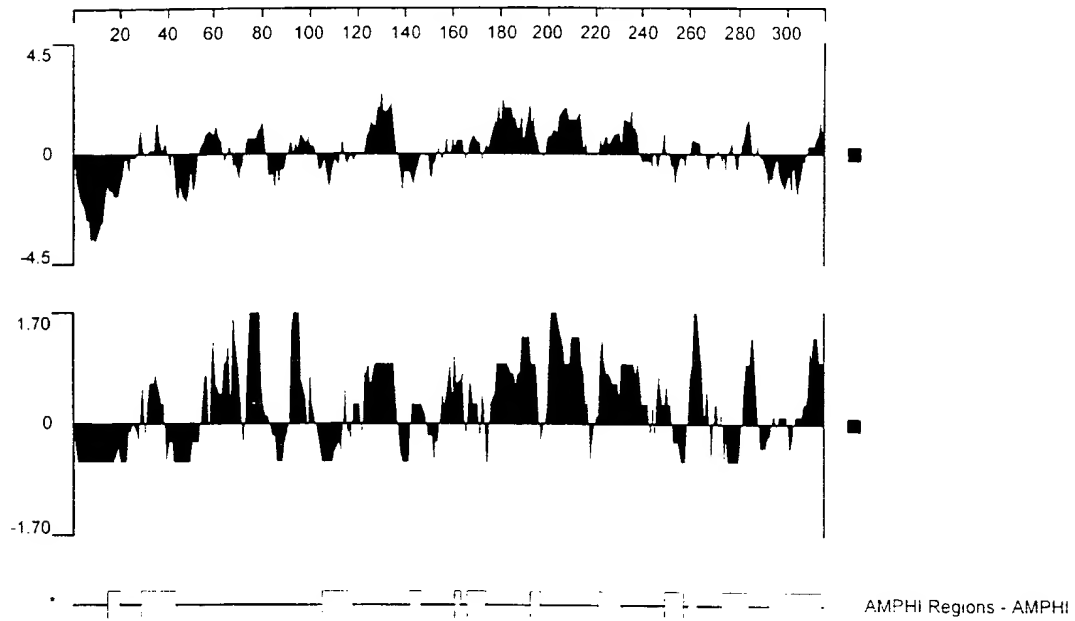
519-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 13

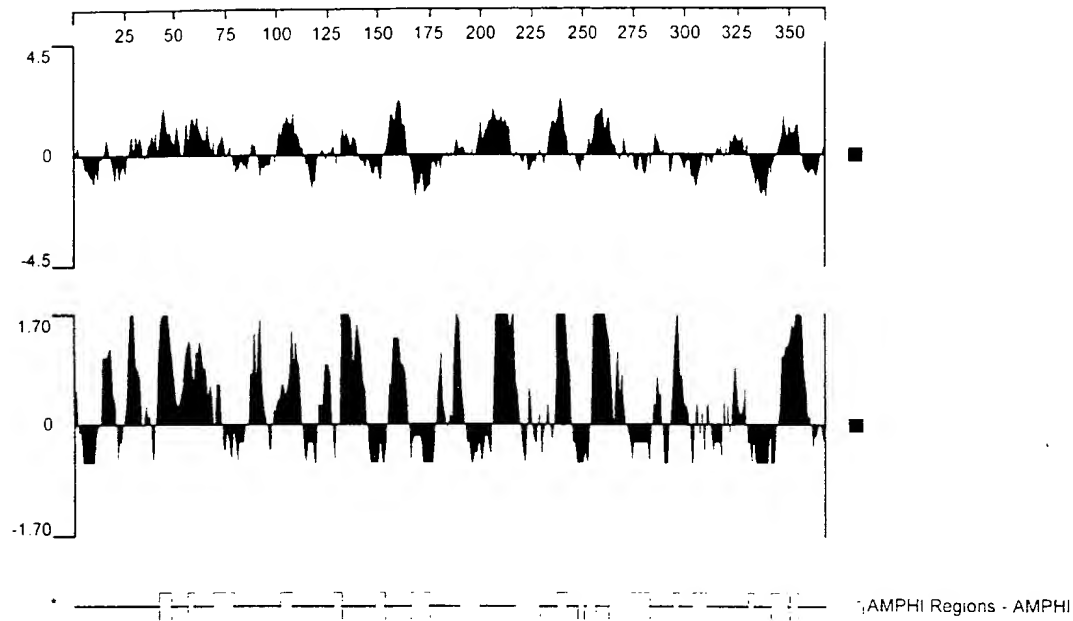
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 14

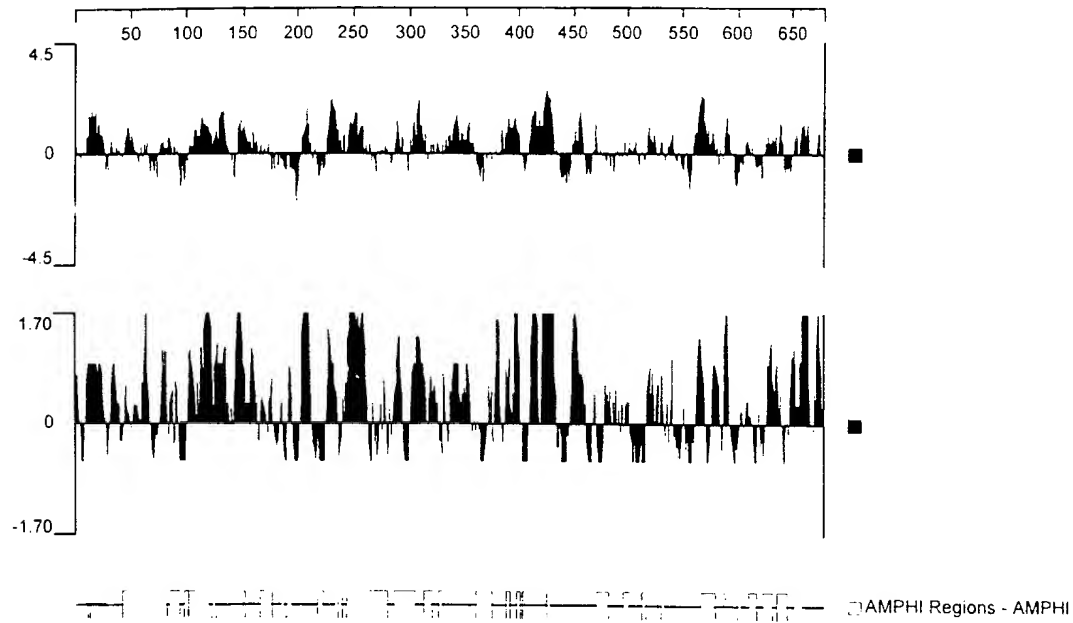
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 15

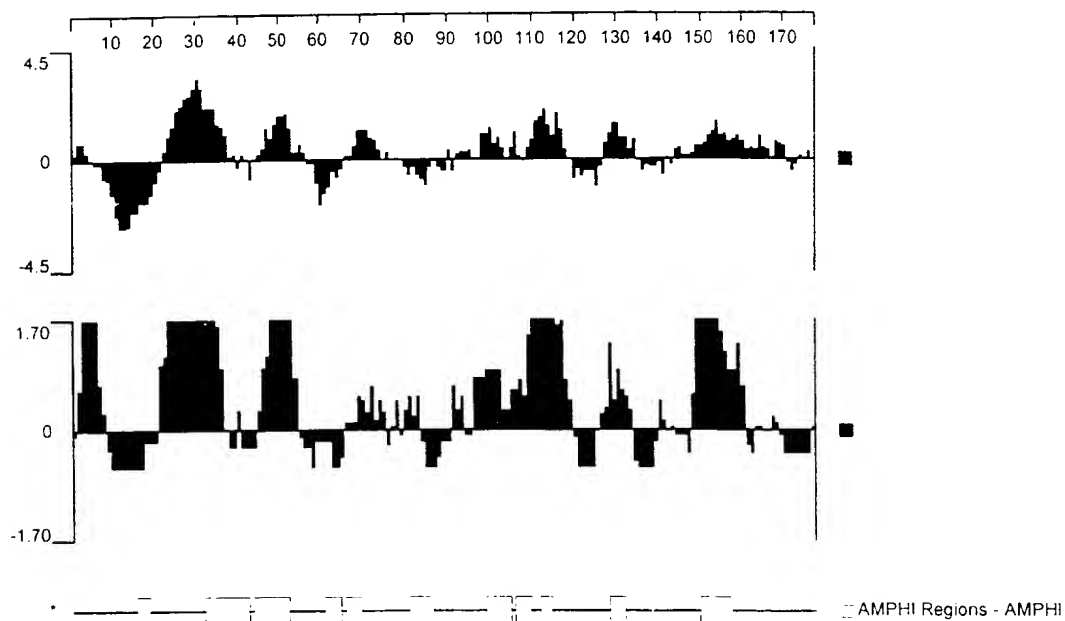
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 16

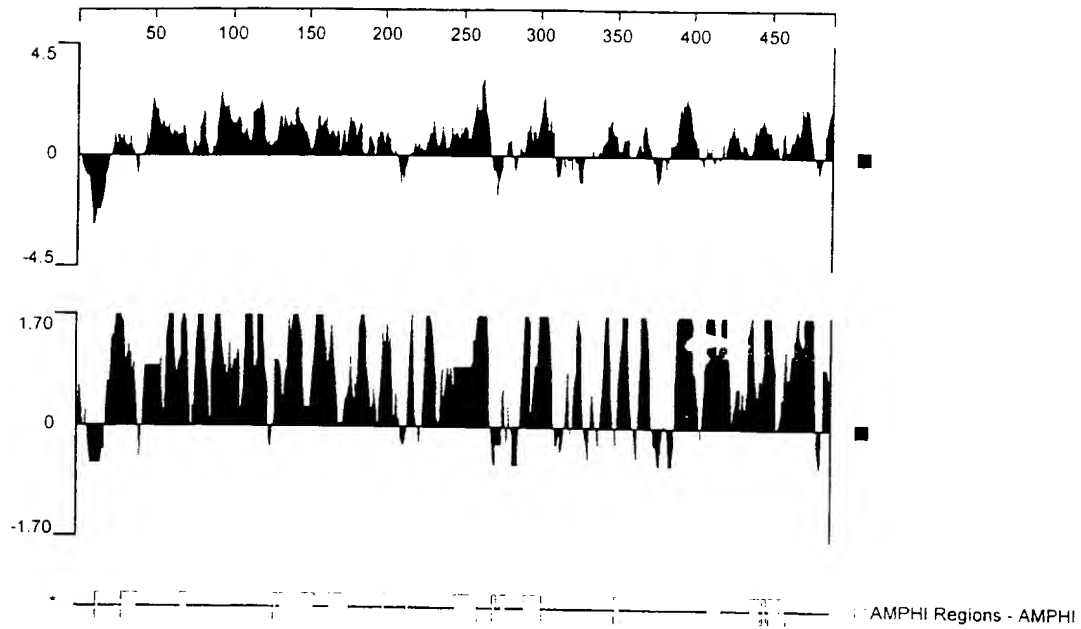
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 17

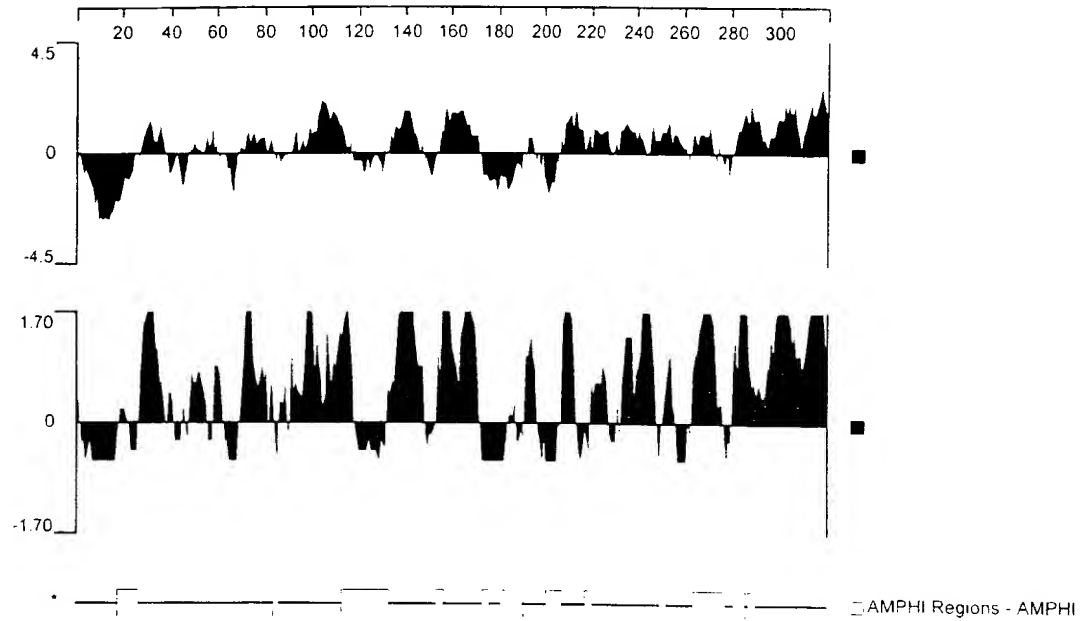
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 18

Fig. 19A

Fig. 19B

zo05_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo08_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
z2491	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo11_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo20_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo01_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo09_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo12_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo22_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo23_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo24_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo25_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo26_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo96_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo02_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo04_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo06_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo07_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
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zo21_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
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zo03_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo15_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
fa1090	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo32_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo33_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*

Fig. 19C

Fig. 20A

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gnmzq09 121 YQILDSVTTVSAKARLVDSRNGKVLWSGSASIREGSNNSNSGLLGALV SAVVNQIANSLT
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fa1090 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALV SAVVNQIANSLT
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gnmzq29 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
z2491 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq14 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq18 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq26 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

```

Fig. 20B

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287_14 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVSE.....KETEAE
287_2 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVSE.....KETEAE
287_21 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVSE.....KETEAE
z2491 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVSE.....KETEAE
287_9 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVSE.....KETEAE
fa1090 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVSE.....KETEAE

287_14 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNDMPQNAADT
287_2 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNDMPQNAADT
287_21 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNDMPQNAADT
z2491 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNDMPQNAADT
287_9 61 VSGAPQADT...QDATAGEGSDMAAVSAENTGNGGAAATDNPKNEDAGAQNDMPQNAADT
fa1090 61 AGGAPQADT...QDATAGEGSDMAAVSAENTGNGGAAATDNPKNEDAGAQNDMPQNAADT

287_14 110 DSLTPNHTPASNMPAGNMENQAPDAGESEOPANQPDMAANTADGMQGGDDPSAGGENAGNTA
287_2 110 DSLTPNHTPASNMPAGNMENQAPDAGESEOPANQPDMAANTADGMQGGDDPSAGGENAGNTA
287_21 110 DSLTPNHTPASNMPAGNMENQAPDAGESEOPANQPDMAANTADGMQGGDDPSAGGENAGNTA
z2491 110 DSLTPNHTPASNMPAGNMENQAPDAGESEOPANQPDMAANTADGMQGGDDPSAGGENAGNTA
287_9 119 DSLTPNHTPASNMPAGNMENQAPDAGESEOPANQPDMAANTADGMQGGDDPSAGGENAGNTA
fa1090 117 .....

287_14 170 AQGTNQAENNOTAGSQNPASSTNPSATNSGGDFGRITNVGNSVVIDGSPSONITLTHCKGDS
287_2 170 AQGTNQAENNOTAGSQNPASSTNPSATNSGGDFGRITNVGNSVVIDGSPSONITLTHCKGDS
287_21 170 AQGTNQAENNOTAGSQNPASSTNPSATNSGGDFGRITNVGNSVVIDGSPSONITLTHCKGDS
z2491 170 AQGTNQAENNOTAGSQNPASSTNPSATNSGGDFGRITNVGNSVVIDGSPSONITLTHCKGDS
287_9 178 DQGTNQAENNOTAGSQNPASSTNPSATNSGGDFGRITNVGNSVVIDGSPSONITLTHCKGDS
fa1090 117 .ESANTGNNQAGSSDSAPABNPAPANGGSDGRITNVGNSVVIDGSPSONITLTHCKGDS

287_14 230 CSGNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNDGKNDKFGVLVADSVMKGINOYII
287_2 230 CSGNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNDGKNDKFGVLVADSVMKGINOYII
287_21 230 CSGNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNDGKNDKFGVLVADSVMKGINOYII
z2491 230 CSGNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNDGKNDKFGVLVADSVMKGINOYII
287_9 238 CDRD.FLDEEAPPKSEFEKLSDAKIKNYKK....DEQRNFGVLVADRVKXGCTNKYII
fa1090 176 CNGDNLDEEAPSKSEFEKLSDAKIKRYKK....DEQRNFGVLVADRVKXGCTNKYII

287_14 290 FYKPKP...TSFARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_2 290 FYKPKP...TSFARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_21 286 FYKPKP...TSFARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
z2491 286 FYKPKP...TSFARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_9 293 IYKDKSASSSARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
fa1090 232 FYTDKEPT.....RSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG

287_14 348 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGREPSRGRFAA
287_2 348 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGREPSRGRFAA
287_21 344 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGREPSRGRFAA
z2491 344 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGREPSRGRFAA
287_9 353 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGREPSRGRFAA
fa1090 285 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGREPSRGRFAA

287_14 408 KVDFGSKSVLDGIIDSGDLHMGTKQKFAAIDGNGFKGTWTENGCGDVSG.FYGPAGEEVA
287_2 408 KVDFGSKSVLDGIIDSGDLHMGTKQKFAAIDGNGFKGTWTENGCGDVSG.FYGPAGEEVA
287_21 404 KVDFGSKSVLDGIIDSGDLHMGTKQKFAAIDGNGFKGTWTENGCGDVSG.FYGPAGEEVA
z2491 404 KVDFGSKSVLDGIIDSGDLHMGTKQKFAAIDGNGFKGTWTENGCGDVSG.FYGPAGEEVA
287_9 413 KVDFGSKSVLDGIIDSGDLHMGTKQKFAAIDGNGFKGTWTENGCGDVSG.FYGPAGEEVA
fa1090 345 KVDFGSKSVLDGIIDSGDLHMGTKQKFAAIDGNGFKGTWTENGCGDVSG.FYGPAGEEVA

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FIG. 21A

287_14	468	GKYSYRPTDAEKGFGVFAGKKEQD*
287_2	468	GKYSYRPTDAEKGFGVFAGKKEQD*
287_21	464	GKYSYRPTDAEKGFGVFAGKKEQD*
z2491	464	GKYSYRPTDAEKGFGVFAGKKEQD*
287_9	473	GKYSYRPTDAEKGFGVFAGKKEQD*
fa1090	405	GKYSYRPTDAEKGFGVFAGKKRD*

FIG. 21B

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z2491_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRAALTAGLNILIPFIDRVAYRHS
zv26_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRAALTAGLNILIPFIDRVAYRHS
zv22_519ass    1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRAALTAGLNILIPFIDRVAYRHS
fa1090_519     1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRAALTAGLNILIPFIDRVAYRHS
zv32_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRAALTAGLNILIPFIDRVAYRHS
zv11_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRAALTAGLNILIPFIDRVAYRHS
zv28_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRAALTAGLNILIPFIDRVAYRHS
zv96_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRAALTAGLNILIPFIDRVAYRHS
zv02_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRAALTAGLNILIPFIDRVAYRHS
zv03_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRAALTAGLNILIPFIDRVAYRHS
zv04_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRAALTAGLNILIPFIDRVAYRHS
zv05_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRAALTAGLNILIPFIDRVAYRHS
zv01_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRAALTAGLNILIPFIDRVAYRHS
zv07_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRAALTAGLNILIPFIDRVAYRHS
zv12_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRAALTAGLNILIPFIDRVAYRHS
zv18_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRAALTAGLNILIPFIDRVAYRHS
zv19_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRAALTAGLNILIPFIDRVAYRHS
zv21_519ass    1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRAALTAGLNILIPFIDRVAYRHS
zv27_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRAALTAGLNILIPFIDRVAYRHS
zv20_519ass    1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRAALTAGLNILIPFIDRVAYRHS
zv06_519ass    1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRAALTAGLNILIPFIDRVAYRHS
zv29_519ass    1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRAALTAGLNILIPFIDRVAYRHS

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z2491_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv26_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv22_519ass    61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
fa1090_519     61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv32_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv11_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv28_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv96_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv02_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv03_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv04_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv05_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv01_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv07_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv12_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv18_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv19_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv21_519ass    61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv27_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv20_519ass    61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv06_519ass    61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv29_519ass    61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG

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z2491_519      121 RMELDKTFEERDEINSTVVSALDEAAGAGWVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv26_519      121 RMELDKTFEERDEINSTVVSALDEAAGAGWVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv22_519ass    121 RMELDKTFEERDEINSTVVSALDEAAGAGWVKVLRYEIKDLVPPQEIILRSMQAQITAERE
fa1090_519     121 RMELDKTFEERDEINSTVVSALDEAAGAGWVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv32_519      121 RMELDKTFEERDEINSTVVSALDEAAGAGWVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv11_519      121 RMELDKTFEERDEINSTVVSALDEAAGAGWVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv28_519      121 RMELDKTFEERDEINSTVVSALDEAAGAGWVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv96_519      121 RMELDKTFEERDEINSTVVSALDEAAGAGWVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv02_519      121 RMELDKTFEERDEINSTVVSALDEAAGAGWVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv03_519      121 RMELDKTFEERDEINSTVVSALDEAAGAGWVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv04_519      121 RMELDKTFEERDEINSTVVSALDEAAGAGWVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv05_519      121 RMELDKTFEERDEINSTVVSALDEAAGAGWVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv01_519      121 RMELDKTFEERDEINSTVVSALDEAAGAGWVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv07_519      121 RMELDKTFEERDEINSTVVSALDEAAGAGWVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv12_519      121 RMELDKTFEERDEINSTVVSALDEAAGAGWVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv18_519      121 RMELDKTFEERDEINSTVVSALDEAAGAGWVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv19_519      121 RMELDKTFEERDEINSTVVSALDEAAGAGWVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv21_519ass    121 RMELDKTFEERDEINSTVVSALDEAAGAGWVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv27_519      121 RMELDKTFEERDEINSTVVSALDEAAGAGWVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv20_519ass    121 RMELDKTFEERDEINSTVVSALDEAAGAGWVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv06_519ass    121 RMELDKTFEERDEINSTVVSALDEAAGAGWVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv29_519ass    121 RMELDKTFEERDEINSTVVSALDEAAGAGWVKVLRYEIKDLVPPQEIILRSMQAQITAERE

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FIG. 22A

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z2491_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv26_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv22_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
fa1090_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv32_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv11_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv28_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv96_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv02_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv03_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv04_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv05_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv01_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv07_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv12_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv18_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv19_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv21_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv27_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv20_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv06_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv29_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR

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z2491_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv26_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv22_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
fa1090_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv32_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv11_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv28_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv96_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv02_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv03_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv04_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv05_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv01_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv07_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv12_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv18_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv19_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv21_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv27_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv20_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv06_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv29_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL

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z2491_519 301 ISAGMKIIDSSKTAK*
zv26_519 301 ISAGMKIIDSSKTAK*
zv22_519ass 301 ISAGMKIIDSSKTAK*
fa1090_519 301 ISAGMKIIDSSKTAK*
zv32_519 301 ISAGMKIIDSSKTAK*
zv11_519 301 ISAGMKIIDSSKTAK*
zv28_519 301 ISAGMKIIDSSKTAK*
zv96_519 301 ISAGMKIIDSSKTAK*
zv02_519 301 ISAGMKIIDSSKTAK*
zv03_519 301 ISAGMKIIDSSKTAK*
zv04_519 301 ISAGMKIIDSSKTAK*
zv05_519 301 ISAGMKIIDSSKTAK*
zv01_519 301 ISAGMKIIDSSKTAK*
zv07_519 301 ISAGMKIIDSSKTAK*
zv12_519 301 ISAGMKIIDSSKTAK*
zv18_519 301 ISAGMKIIDSSKTAK*
zv19_519 301 ISAGMKIIDSSKTAK*
zv21_519ass 301 ISAGMKIIDSSKTAK*
zv27_519 301 ISAGMKIIDSSKTAK*
zv20_519ass 301 ISAGMKIIDSSKTAK*
zv06_519ass 301 ISAGMKIIDSSKTAK*
zv29_519ass 301 ISAGMKIIDSSKTAK*

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Fig. 22B

Fig. 23A

Fig. 23B

Fig. 23C

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fa1090 361 IDRRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm33asbc 361 IDRRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm32asbc 361 IDRRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm23asbc 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm27bc 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm09 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm10 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm24 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm25 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm14 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm04 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm11asbc 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm08n 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm96 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm01 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm02 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm03 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm07 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm12 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm18 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm19 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm20 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm21 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm06 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm17 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm13 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm05 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
z2491 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm22 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm26 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm28 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm29asbc 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm16 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm15 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm31asbc 361 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK

fa1090 421 QKTTGYVWQLLPNGMKPEYRP*
zm33asbc 421 QKTTGYVWQLLPNGMKPEYRP*
zm32asbc 421 QKTTGYVWQLLPNGMKPEYRP*
zm23asbc 421 QKTTGYVWQLLPNGMKPEYRP*
zm27bc 421 QKTTGYVWQLLPNGMKPEYRP*
zm09 421 QKTTGYVWQLLPNGMKPEYRP*
zm10 421 QKTTGYVWQLLPNGMKPEYRP*
zm24 421 QKTTGYVWQLLPNGMKPEYRP*
zm25 421 QKTTGYVWQLLPNGMKPEYRP*
zm14 421 QKTTGYVWQLLPNGMKPEYRP*
zm04 421 QKTTGYVWQLLPNGMKPEYRP*
zm11asbc 421 QKTTGYVWQLLPNGMKPEYRP*
zm08n 421 QKTTGYVWQLLPNGMKPEYRP*
zm96 421 QKTTGYVWQLLPNGMKPEYRP*
zm01 421 QKTTGYVWQLLPNGMKPEYRP*
zm02 421 QKTTGYVWQLLPNGMKPEYRP*
zm03 421 QKTTGYVWQLLPNGMKPEYRP*
zm07 421 QKTTGYVWQLLPNGMKPEYRP*
zm12 421 QKTTGYVWQLLPNGMKPEYRP*
zm18 421 QKTTGYVWQLLPNGMKPEYRP*
zm19 421 QKTTGYVWQLLPNGMKPEYRP*
zm20 421 QKTTGYVWQLLPNGMKPEYRP*
zm21 421 QKTTGYVWQLLPNGMKPEYRP*
zm06 421 QKTTGYVWQLLPNGMKPEYRP*
zm17 421 QKTTGYVWQLLPNGMKPEYRP*
zm13 421 QKTTGYVWQLLPNGMKPEYRP*
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zm26 421 QKTTGYVWQLLPNGMKPEYRP*
zm28 421 QKTTGYVWQLLPNGMKPEYRP*
zm29asbc 421 QKTTGYVWQLLPNGMKPEYRP*
zm16 421 QKTTGYVWQLLPNGMKPEYRP*
zm15 421 QKTTGYVWQLLPNGMKPEYRP*
zm31asbc 421 QKTTGYVWQLLPNGMKPEYRP*

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Fig. 23D